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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:26:03 ; Search time 132.37 Seconds  
(without alignments)  
6266.684 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

Sequence: 1 actacacacactccactgc.....ttctgtgtagtgaccgt 385

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3050214 seqs, 1077301958 residues

Total number of hits satisfying chosen parameters: 6100428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	100.0	385	7	US-11-344-932-67
2	385	100.0	385	10	US-11-349-541-67
3	307.2	79.8	3228	7	US-11-344-932-701
4	231.8	60.2	1016	8	US-11-266-748A-350613
5	231.8	60.2	1016	8	US-11-266-748A-383047
6	231.8	60.2	1016	8	US-11-266-748A-433992
7	107.4	27.9	2841	7	US-11-344-932-700
8	95	24.7	1016	8	US-11-266-748A-350613
9	95	24.7	1016	8	US-11-266-748A-383047
10	95	24.7	1016	8	US-11-266-748A-433992
11	89.2	23.2	5449	8	US-11-266-748A-32477
12	84	21.8	385	7	US-11-344-932-67
13	84	21.8	385	10	US-11-349-541-67
14	77.2	20.1	25694	6	US-10-669-920-46
15	75.2	19.5	154394	8	US-11-266-748A-58517
16	73.8	19.2	80988	6	US-10-669-920-261
17	73.8	19.2	421987	8	US-11-266-748A-28210
18	70.4	18.3	3228	7	US-11-344-932-701
19	69.6	18.1	593	8	US-11-266-748A-254460
20	67.6	17.6	198285	8	US-11-266-748A-314977
21	67.6	17.6	198285	8	US-11-266-748A-59857
22	67.6	17.6	4647455	6	US-10-641-321-205

23	64.2	16.7	219955	7	US-11-371-354-11185	Sequence 11185, A
24	63.8	16.6	755217	8	US-11-266-748A-29045	Sequence 29045, A
25	62.6	16.3	1000	8	US-11-266-748A-200795	Sequence 200795, A
26	62.6	16.3	1550	7	US-11-371-354-11257	Sequence 11257, A
27	62.6	16.3	1550	8	US-11-266-748A-57638	Sequence 57638, A
28	60	15.6	2841	7	US-11-344-932-700	Sequence 700, App
29	59.2	15.4	1237661	8	US-11-266-748A-29041	Sequence 29041, A
30	59	15.3	1071650	8	US-11-266-748A-22664	Sequence 22664, A
31	58.8	15.3	166949	8	US-11-266-748A-60144	Sequence 60144, A
32	53.2	13.8	1000	8	US-11-266-748A-196189	Sequence 196189, A
33	53	13.8	327636	10	US-11-073-360-1613	Sequence 1613, Ap
34	52	13.5	96618	8	US-11-266-748A-24171	Sequence 24171, A
35	51.6	13.4	1237661	8	US-11-266-748A-29041	Sequence 29041, A
36	50.2	13.0	1550	7	US-11-371-354-11257	Sequence 11257, A
37	50.2	13.0	1550	8	US-11-266-748A-57638	Sequence 57638, A
38	49.8	12.9	421987	8	US-11-266-748A-28210	Sequence 28210, A
39	49.4	12.8	420555	6	US-10-669-920-1140	Sequence 1140, Ap
40	49.4	12.6	1000	8	US-11-266-748A-203066	Sequence 203066, A
41	48.4	12.5	2051	7	US-11-344-932-699	Sequence 699, App
42	48	12.5	2051	8	US-11-266-748A-32477	Sequence 32477, A
43	48	12.5	5449	8	US-11-330-648-22	Sequence 22, Appl
44	47.4	12.3	31670	10	US-11-330-648-22	Sequence 4, Appli
45	47.4	12.3	31704	6	US-10-669-920-4	

ALIGNMENTS

RESULT 1

US-11-344-932-67  
; Sequence 67, Application US/11344932  
; Publication NO. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Deng, Fa  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C32  
; CURRENT APPLICATION NUMBER: US/11/344,932  
; PRIOR FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: 10/144,678  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 10/012,896  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 09/895,814  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/852,911  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: 09/780,669  
; PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-67

Query Match      100.0%; Score 385; DB 7; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.9e-119;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCGCCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCGCCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCGAGCAGACATCATGAGGTTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCGAGCAGACATCATGAGGTTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGTCGAGATTTCATTTTGAGAGAGTCTCTCTGAGACCTGTATCTTTAGAGG 240
Db 181 TGTGCTGTGTCGAGATTTCATTTTGAGAGAGTCTCTCTGAGACCTGTATCTTTAGAGG 240
Qy 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGACCTCTTGTAGTCTGCTTG 300
Db 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGACCTCTTGTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTCTGCTTACAGGGCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 2
US-11-349-541-67
; Sequence 67, Application US/11349541
; Publication No. US20060223129A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

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; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-349-541-67

Query Match      100.0%; Score 385; DB 10; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.9e-119;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCGCCAGCACTTTAGGAATGCTGA 60
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Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCGAGCAGACATCATGAGGTTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCCGAGCAGACATCATGAGGTTTC 120
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGTCGAGATTTCATTTTGAGAGAGTCTCTCTGAGACCTGTATCTTTAGAGG 240
Db 181 TGTGCTGTGTCGAGATTTCATTTTGAGAGAGTCTCTCTGAGACCTGTATCTTTAGAGG 240
Qy 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGACCTCTTGTAGTCTGCTTG 300
Db 241 CTGGGACAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGACCTCTTGTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTCTGCTTACAGGGCACTCTCAGATGCCATAC 360
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Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3
US-11-344-932-701
; Sequence 701, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
;; FILE REFERENCE: 210121.427C32  
;; CURRENT APPLICATION NUMBER: US/11/344,932  
;; CURRENT FILING DATE: 2006-02-01  
;; PRIOR APPLICATION NUMBER: 10/144,678  
;; PRIOR FILING DATE: 2002-05-09  
;; PRIOR APPLICATION NUMBER: 10/012,896  
;; PRIOR FILING DATE: 2001-12-10  
;; PRIOR APPLICATION NUMBER: 09/895,814  
;; PRIOR FILING DATE: 2001-06-29  
;; PRIOR APPLICATION NUMBER: 09/852,911  
;; PRIOR FILING DATE: 2001-05-09  
;; PRIOR APPLICATION NUMBER: 09/780,669  
;; PRIOR FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: 09/759,143  
;; PRIOR FILING DATE: 2001-01-12  
;; PRIOR APPLICATION NUMBER: 09/709,729  
;; PRIOR FILING DATE: 2000-11-09  
;; PRIOR APPLICATION NUMBER: 09/685,166  
;; PRIOR FILING DATE: 2000-10-10  
;; PRIOR APPLICATION NUMBER: 09/679,426  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 09/657,279  
;; PRIOR FILING DATE: 2000-09-06  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 1033  
;; SOFTWARE: Fast-Seq for Windows Version 3.0  
;; SEQ ID NO 701  
;; LENGTH: 3228  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: 66, 2343, 2387, 3065  
;; OTHER INFORMATION: n = A,T,C or G  
US-11-344-932-701

Query Match 79.8%; Score 307.2; DB 7; Length 3228;  
Best Local Similarity 92.0%; Pred. No. 1.4e-92;  
Matches 346; Conservative 0; Mismatches 28; Indels 2; Gaps 2;  
  
QY 12 TCCACTTGGCCCTTGTGAGACACTTTGTCCAGACACTTTAGGAATGCTGAGGTCGGACCA 71  
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QY 72 CCACATCTCATGTCAGAGATGCCCCAGACATCAGCTCAGAGTCCCTTTT-AA 130  
Db 352 CCACATCTTATATGCAAGATGCCCCAGAGATCAGGTCAGAGTTCCTTTTAA 411  
  
QY 131 AAAGGGGACTTGTCTTAA-AAAGAGTCTAGCCACGATTTGTAGAGCAGCTGTGTG 189  
Db 412 AAAGGAGACTTGTCTTAAATAAAGAGTCTAGCCACGTTGTGTAGAGCGCTGTGTG 471  
  
QY 190 CTGGAGATTCACATTTTGTGAGAGTCTCTCTCTGAGACCTGATCTTTAGAGGCTGGCAGT 249  
Db 472 CTGGGGTTTACATTTTGTGAGAGTCTCTCTCTGAGACCTGATCTCTGGAGGCTGGGCAAT 531  
  
QY 250 CTTCACATGAGATGGGGCTGGTCTGATCTCAGACCTCTTGTCTGTCTGTCTCTCCCA 309  
Db 532 CTTCGCACTTGTGATGGGGCTGGTCTGATCTCAGACCTCTTGTCTGTCTGTCTCTCCCA 591  
  
QY 310 GGCCCCCAGCTGGCCACACCTGTTACAGGGGCACTCTCAGATGCCATACCATGTTTC 369  
Db 592 TGGCCCCAGCTGGCCACACCTGTTACGGGGCACTCTTAGATGCCACACCATGTTTC 651  
  
QY 370 TGTGCTAGTGGACCGT 385  
Db 652 CATGCTAGTGGACTGT 667

RESULT 4  
US-11-266-748A-350613/c  
; Sequence 350613, Application US/11566748A

;; Publication No. US20060134663A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Harkin, Paul  
;; APPLICANT: Johnston, Patrick  
;; APPLICANT: Mulligan, Karl  
;; TITLE OF INVENTION: Transcriptome Microarray Technology and  
;; TITLE OF INVENTION: Methods of Using the Same  
;; FILE REFERENCE: 55815-0102 (319189)  
;; CURRENT APPLICATION NUMBER: US/11/266,748A  
;; CURRENT FILING DATE: 2005-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105479.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105482.6  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105483.4  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105507.0  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105485.9  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105484.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: US 60/662,276  
;; PRIOR FILING DATE: 2005-03-14  
;; PRIOR APPLICATION NUMBER: US 60/700,293  
;; PRIOR FILING DATE: 2005-07-18  
;; NUMBER OF SEQ ID NOS: 483996  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 350613  
;; LENGTH: 1016  
;; TYPE: DNA  
;; ORGANISM: Homo Sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (860)..(881)  
;; OTHER INFORMATION: n is a, c, g, or t  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (964)..(972)  
;; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-350613

Query Match 60.2%; Score 231.8; DB 8; Length 1016;  
Best Local Similarity 88.0%; Pred. No. 1.9e-67;  
Matches 265; Conservative 0; Mismatches 32; Indels 4; Gaps 1;  
  
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Db 442 CTCACATTCCTTGTGAGATCTTTATCCAGCACTTTAGGAATGCTAAAGTTCAGATCA 383  
  
QY 71 GCCACATCTCATGTCAGAGATTTGCCAGACATCAGCTGAGAGTTCCTTTTAAA 130  
Db 382 GCCCATCTCATGTTCAAGACTGCCAGAGATCAGTTCAGAGTTCCTTTCAA 323  
  
QY 131 AAAGGGGACTTCTCTTAAAAAAGAGTCTAGCCACGATTTGTAGAGCAGCTGTGTGTC 190  
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QY 191 TCGAGATTCACATTTTGTGAGAGATTTCTCTCTGAGACCTGATCTTTAGAGGCTGGGAGTC 250  
Db 262 CGGGGGTTCACATTTTGTGAGACAGTTCCTCTCTGAGACCTGATCTCT- 207  
  
QY 251 TTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCTTCTAGTCTGCTGCTCTCCCA 310  
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QY 311 G 311  
Db 146 G 146

RESULT 5  
US-11-266-748A-383047/c

; Sequence 383047, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 383047  
; LENGTH: 1016  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (880)..(881)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (964)..(972)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-383047

Query Match 60.2%; Score 231.8; DB 8; Length 1016;  
Best Local Similarity 88.0%; Pred. No. 1.9e-67;  
Matches 265; Conservative 0; Mismatches 32; Indels 4; Gaps 1;  
Qy 11 CTCACATCTCATGTGCAAGATTGCCAGCAGATCAGGTCTGAGAGTTCCTCTTTAA 70  
Db 442 CTCACGTGCTTTGTGAGATCTTTATCCAGCAGCTTTAGGAATGCTAGGTGCGACCA 383  
Qy 71 GCCACATCTCATGTGCAAGATTGCCAGCAGATCAGGTCTGAGAGTTCCTCTTTAA 130  
Db 382 GCCCATCTCATGTTCAAGACTGCCAGCAGAGATCAGTTCACAGATTCCTCTTCAA 323  
Qy 131 AAAGGGGACTTGGCTTAAAGAAAGTCTAGCCAGCAGATGTTGAGAGCAGCTGTGCTGTC 190  
Db 322 AAAGGGGACTTGGCTTAAAGAAAGTCTAGCCATGTTGTGTAAGCAGCTATGCTGTC 263  
Qy 191 TGGAGATTACATTTTGTGAGAGTCTCTCTGAGACCTGATCTTTAGAGGCTGGGCACTC 250  
Db 262 CGGGGGTTTCACTTTTGTGAGACAGTCTCTCTGAGACCTGATCTCT---GCTGGGCACTC 207  
Qy 251 TTGCACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTCTAGTCTGCTTGCCTCTCCAG 310  
Db 206 CTGCACATGAGATGGGGCTGGTCTGATATCAGCAGCTCTCCCTAGTCTGCTTGCCTCTCCAG 147  
Qy 311 G 311  
Db 146 G 146

US-11-266-748A-433992  
; Sequence 433992, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 433992  
; LENGTH: 1016  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (45)..(53)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (136)..(137)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-433992

Query Match 60.2%; Score 231.8; DB 8; Length 1016;  
Best Local Similarity 88.0%; Pred. No. 1.9e-67;  
Matches 265; Conservative 0; Mismatches 32; Indels 4; Gaps 1;  
Qy 11 CTCACATCTCATGTGCAAGATTGCCAGCAGATCAGGTCTGAGAGTTCCTCTTTAA 70  
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Qy 71 GCCACATCTCATGTGCAAGATTGCCAGCAGATCAGGTCTGAGAGTTCCTCTTTAA 130  
Db 635 GCCCATCTCATGTTCAAGACTGCCAGCAGAGATCAGTTCACAGATTCCTCTTCAA 694  
Qy 131 AAAGGGGACTTGGCTTAAAGAAAGTCTAGCCAGCAGATGTTGAGAGCAGCTGTGCTGTC 190  
Db 695 AAAGGGGACTTGGCTTAAAGAAAGTCTAGCCATGTTGTGTAAGCAGCTATGCTGTC 754  
Qy 191 TGGAGATTACATTTTGTGAGAGTCTCTCTGAGACCTGATCTTTAGAGGCTGGGCACTC 250  
Db 755 CGGGGGTTTCACTTTTGTGAGACAGTCTCTCTGAGACCTGATCTCT---GCTGGGCACTC 810  
Qy 251 TTGCACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTCTAGTCTGCTTGCCTCTCCAG 310  
Db 811 CTGCACATGAGATGGGGCTGGTCTGATATCAGCAGCTCTCCCTAGTCTGCTTGCCTCTCCAG 870  
Qy 311 G 311  
Db 871 G 871





QY 291 A 291  
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DB 405 A 405

RESULT 9  
US-11-266-748A-383047  
; Sequence 383047, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 383047  
; LENGTH: 1016  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (880)..(881)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (964)..(972)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-383047

Query Match 24.7%; Score 95; DB 8; Length 1016;  
Best Local Similarity 65.1%; Pred. No. 2.2e-21;  
Matches 157; Conservative 0; Mismatches 80; Indels 4; Gaps 1;  
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DB 169 GGAGTGTGATATCAGACAGCCATCTCATGTGCAAGATTGCCAGCAGACATCAGGT 228  
QY 111 CTGAGAGTCCCTTTTAAAGAGGGGACTTGTCTTAAAGAGGAGTCTAGCCACGATTGT 170  
DB 229 CTCAGAGGAGACTGTCTCAAGAGTGAACCCCGGACAGCATAGCTGCTTTACACAAC 288  
QY 171 GTAGAGCAGCTGTGCTGTGAGATTTCATCTTTTGTAGAGAGTTCTCTCTGTGAGACCTGA 230  
DB 289 ATGGCCAGGCTTCTTTTGTAGCAAGTCCCTTTTGAAGAGGGGAACTCTGGAAGTGA 348  
QY 231 TCTTTAGAGGCTGGGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCCTT 290  
DB 349 TCTCT----GCTGGGAGTCTTGAACATGAGATGGGGCTGATCTGAACCTTAGCATTCCTA 404  
QY 291 A 291  
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DB 405 A 405

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US-11-266-748A-433992/c  
; Sequence 433992, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 433992  
; LENGTH: 1016  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (45)..(53)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (136)..(137)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-433992  
Query Match 24.7%; Score 95; DB 8; Length 1016;  
Best Local Similarity 65.1%; Pred. No. 2.2e-21;  
Matches 157; Conservative 0; Mismatches 80; Indels 4; Gaps 1;  
QY 51 GGAATGCTGAGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGT 110  
DB 848 GGAGTGTGATATCAGACAGCCATCTCATGTGCAAGATTGCCAGCAGACATCAGGT 789  
QY 111 CTGAGAGTCCCTTTTAAAGAGGGGACTTGTCTTAAAGAGGAGTCTAGCCACGATTGT 170  
DB 788 CTCAGAGGAGAACTGTCTCAAGAGTGAACCCCGGACAGCATAGCTGCTTTACACAAC 729  
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DB 612 A 612

RESULT 11

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; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-67

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Best Local Similarity 64.5%; Pred. No. 6.7e-18;
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Qy 164 CGATTGTGTAGACGACGCTGTCTGTGCTGGAGATTCACCTTTTGAAGAGAGTTCTCCTCTGA 223
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Qy 224 GACCTGATCTTTTAGAGGCTGGCAGTCTTGCACATGATGAGATGGGGCTGGTCTGATCTCAGC 283
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Qy 284 ACTCCTTA 291
Db 55 ATTCCTAA 48

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; Sequence 67, Application US/11349541
; Publication No. US20060223129A1

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QY 300 GCCTCTCCCAAGGCGCCCGAGCTGGCCACACCTGCTTACAGGGCA 343  
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Job time : 139.37 secs

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Run on: December 31, 2006, 12:22:01 ; Search time 613.045 Seconds  
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Perfect score: 385  
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Gapop 10.0 , Gapext 1.0  
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Total number of hits satisfying chosen parameters: 37784340  
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Maximum Match 100%  
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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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Result No.	Score	Match	Length	DB	ID	Score	Match	Length	DB	ID	Score	Match	Length	DB	ID
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3	385	100.0	385	3	US-09-822-827-701	Sequence 701, App	Sequence 701, App	Sequence 701, App	Sequence 701, App	Sequence 701, App	Sequence 701, App	Sequence 701, App	Sequence 701, App	Sequence 701, App	Sequence 701, App
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ALIGNMENTS

RESULT 1

US-09-759-143-67  
; Sequence 67, Application US/09759143  
; Patent No. US2002022248A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Jennifer L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-759-143-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 ACTACACACTCCACTTGGCCCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60  
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## RESULT 2

US-09-780-669-67

; Sequence 67, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-780-669-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 3

US-09-030-606-67

; Sequence 67, Application US/09030606

; Patent No. US20020081580A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F

; NUMBER OF SEQUENCES: 224

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/030,606

; FILING DATE: 25-FEB-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.428C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 67:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 385 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

US-09-030-606-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy	1	ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCACTTTAGGAATGCTGA	60
Db	1	ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCACTTTAGGAATGCTGA	60
Qy	61	GGTCGGACCAGCCACCATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTCAGAGTTC	120
Db	61	GGTCGGACCAGCCACCATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTCAGAGTTC	120
Qy	121	CCCTTTTAAAAAAGGGGACTTGCCTTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGACGAG	180
Db	121	CCCTTTTAAAAAAGGGGACTTGCCTTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGACGAG	180
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTCTCCTCTGAGACCTGATCTTTTAGAG	240
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTCTCCTCTGAGACCTGATCTTTTAGAG	240
Qy	241	CTGGGCAGCTTGCACATGAGATGGGGCTGCTGATCTCAGGCACCTCCTTAGTCTGCTTG	300
Db	241	CTGGGCAGCTTGCACATGAGATGGGGCTGCTGATCTCAGGCACCTCCTTAGTCTGCTTG	300
Qy	301	CCTCTCCCAAGGGCCCCAGCCTGGCCACACCTTGCCTTACAGGGCACTCTCAGATGCCCATAC	360
Db	301	CCTCTCCCAAGGGCCCCAGCCTGGCCACACCTTGCCTTACAGGGCACTCTCAGATGCCCATAC	360
Qy	361	CATAGTTTCTGTGCTAGTGGACCGT	385
Db	361	CATAGTTTCTGTGCTAGTGGACCGT	385

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RESULT 4
US-09-822-827-67
; Sequence 67, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: XU, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-67

```

Query Match	100.0%;	Score 385;	DB 3;	Length 385;
Best Local Similarity	100.0%;	Pred. No. 2.2e-126;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy 1	ACTACACACACTCCACTTGGCCCTTGAGAGACACTTTGTC	CCAGCAGCACTTTAGGAATCCTGA	60	
Db 1	ACTACACACACTCCACTTGGCCCTTGAGAGACACTTTGTC	CCAGCAGCACTTTAGGAATCCTGA	60	
Qy 61	GGTCGAGCAGGCACATCTCATGTGCAAGATTGCCAGCAGACAT	CAGGTCCTCAGAGTTC	120	
Db 61	GGTCGAGCAGGCACATCTCATGTGCAAGATTGCCAGCAGACAT	CAGGTCCTCAGAGTTC	120	
Qy 121	CCCTTTTAAAAAAGGGGACTTGCTTTAAAAAAGAGTCTAGCCACGAT	TGTGTAGACGAC	180	
Db 121	CCCTTTTAAAAAAGGGGACTTGCTTTAAAAAAGAGTCTAGCCACGAT	TGTGTAGACGAC	180	
Qy 181	TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGAC	CTGATCTTTAGAGG	240	
Db 181	TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGAC	CTGATCTTTAGAGG	240	
Qy 241	CTGGGCGAGTCTGCACATGAGATGGGCTGCTCGATCTCAGACACT	CTCTTAGTCTCCTTG	300	
Db 241	CTGGGCGAGTCTGCACATGAGATGGGCTGCTCGATCTCAGACACT	CTCTTAGTCTCCTTG	300	
Qy 301	CCTCTCCAGGGCCCCAGCCTGGCCACACCTTGCTTTACAGGGCACT	CTTCAGATCCCCATAC	360	

```

|||||
Db      301  CCTCTCCAGGGCCCCAGCTGGCCACCTGCTTACAGGCACTCTCAGATGCCCATAC 360
|||||
Qy      361  CATAGTTTCTGCTGCTAGTGGACCGT 385
|||||
Db      361  CATAGTTTCTGCTGCTAGTGGACCGT 385
|||||

RESULT 5
US-09-115-453-67
: Sequence 67, Application US/09115453B
: Patent No. US20020090372A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
: TITLE OF INVENTION: METHODS FOR THEIR USE
: FILE REFERENCE: 210121.427C4
: CURRENT APPLICATION NUMBER: US/09/115.453B
: CURRENT FILING DATE: 1998-07-14
: NUMBER OF SEQ ID NOS: 228
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 67
: LENGTH: 385
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-115-453-67

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RESULT 6  
US-09-232-880-67  
; Sequence 67, Application US/09232880  
; Publication No. US200182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.4280C  
; CURRENT APPLICATION NUMBER: US/09/232.880.

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; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60
   |||
Db 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60
   |||

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTAGAGTTTC 120
   |||
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTAGAGTTTC 120
   |||

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||

Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||

Qy 241 CTGGGCACTTGTGCACATGAGATGGGCTGTGCTGATCTCAGACCTCTCTAGTCTGCTTG 300
   |||
Db 241 CTGGGCACTTGTGCACATGAGATGGGCTGTGCTGATCTCAGACCTCTCTAGTCTGCTTG 300
   |||

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
   |||
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
   |||

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
   |||
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
   |||

RESULT 7
US-09-895-793-67
; Sequence 67, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60
   |||
Db 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTTGTCCAGACACTTTAGGAATGCTGA 60
   |||

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTAGAGTTTC 120
   |||
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCGTAGAGTTTC 120
   |||

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||

Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||

Qy 241 CTGGGCACTTGTGCACATGAGATGGGCTGTGCTGATCTCAGACCTCTCTAGTCTGCTTG 300
   |||
Db 241 CTGGGCACTTGTGCACATGAGATGGGCTGTGCTGATCTCAGACCTCTCTAGTCTGCTTG 300
   |||

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
   |||
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360
   |||

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
   |||
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
   |||

RESULT 8
US-09-895-814-67
; Sequence 67, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
```

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; FILE REFERENCE: 210121.427C27
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-67
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Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
   |||||
Db 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
   |||||

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
   |||||
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
   |||||

QY 121 CCTTTTAAAAAGGGGACTTGCCTTAAAGAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||||
Db 121 CCTTTTAAAAAGGGGACTTGCCTTAAAGAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||||

QY 181 TGTGCTGTGCTGAGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||||
Db 181 TGTGCTGTGCTGAGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||||

QY 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTTAGTCTGCTTG 300
   |||||
Db 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTTAGTCTGCTTG 300
   |||||

QY 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
   |||||
Db 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
   |||||

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
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RESULT 9
US-10-012-896-67
; Sequence 67, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
```

```
; FILE REFERENCE: 210121.427C27
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-67

Query Match      100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
   |||||
Db 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
   |||||

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
   |||||
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120
   |||||

QY 121 CCTTTTAAAAAGGGGACTTGCCTTAAAGAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||||
Db 121 CCTTTTAAAAAGGGGACTTGCCTTAAAGAGAGTCTAGCCAGATTGTGTAGAGCAGC 180
   |||||

QY 181 TGTGCTGTGCTGAGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||||
Db 181 TGTGCTGTGCTGAGAGATTCACTTTTGGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
   |||||

QY 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTTAGTCTGCTTG 300
   |||||
Db 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGACCTCCTTTAGTCTGCTTG 300
   |||||

QY 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
   |||||
Db 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
   |||||

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
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```
RESULT 10
US-10-010-940-67
; Sequence 67, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-010-940-67
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Query Match 100.0%; Score 385; DB 6; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126; Indels 0; Gaps 0;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCAGCACTTTTAGGAATGCTGA 60  
Dy 1 ACTACACACTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCAGCACTTTTAGGAATGCTGA 60

Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120  
Dy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120

Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATGCTGAGAGCAGC 180  
Dy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATGCTGAGAGCAGC 180

Qy 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCCTCTGAGACCTGATCTTTTAGAGG 240  
Dy 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCCTCTGAGACCTGATCTTTTAGAGG 240

Qy 241 CTGGCAGCTTGGCAGATGAGATGGGGCTGTGTGATCTGAGCACTCCTTTAGTCTGCTTG 300  
Dy 241 CTGGCAGCTTGGCAGATGAGATGGGGCTGTGTGATCTGAGCACTCCTTTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360  
Dy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
Dy 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 11

US-10-144-678A-67

; Sequence 67, Application US/10144678A

; Publication No. US20030157089A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yudi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A. W.

; APPLICANT: Hepler, William T.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals y de Bassols, Carlota

; APPLICANT: Foy, Teresa M.

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Deng, Ta

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C28

; CURRENT APPLICATION NUMBER: US/10/144,678A

; CURRENT FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 1033

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-144-678A-67

Query Match 100.0%; Score 385; DB 7; Length 385;

Best Local Similarity 100.0%; Pred. No. 2.2e-126;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 12

US-10-294-025-67

; Sequence 67, Application US/10294025

; Publication No. US20030185830A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Stolk, John A.

; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C29

; CURRENT APPLICATION NUMBER: US/10/294,025

; CURRENT FILING DATE: 2002-11-12

; NUMBER OF SEQ ID NOS: 1038

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-294-025-67

Query Match 100.0%; Score 385; DB 7; Length 385;

Best Local Similarity 100.0%; Pred. No. 2.2e-126;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	181	TTGCTGTGCTGGAGATTCATTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG	240
Qy	241	CTGGCGAGTCTTTGCACATGAGATGGGGCTGTCTGATCTCAGCACTCCTTAGTCTGCTTG	300
Db	241	CTGGCGAGTCTTTGCACATGAGATGGGGCTGTCTGATCTCAGCACTCCTTAGTCTGCTTG	300
Qy	301	CCTCTCCAGGGCCCCAGGCTTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC	360
Db	301	CCTCTCCAGGGCCCCAGGCTTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC	360
Qy	361	CATAGTTTCTGTGCTAGTGGACCGT	385
Db	361	CATAGTTTCTGTGCTAGTGGACCGT	385

RESULT 13

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US-10-688-838-67
; Sequence 67, Application US/10688838
; Publication No. US20040141989A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D4
; CURRENT APPLICATION NUMBER: US/10/688,838
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-688-838-67

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Query Match      100.0%; Score 385; DB 8; Length 385;
Best_Local_Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	ACTACACACACTCCACTTGCCTTGTGAGACACATTTGTCCAGACACTTTAGGAATGCTGA	60
Db	1	ACTACACACACTCCACTTGCCTTGTGAGACACATTTGTCCAGACACTTTAGGAATGCTGA	60
Qy	61	GGTCGGACCAAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC	120
Db	61	GGTCGGACCAAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC	120
Qy	121	CCCTTTTAAAAAAGGGGACCTTGCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC	180
Db	121	CCCTTTTAAAAAAGGGGACCTTGCTTAAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC	180
Qy	181	TGTGCTGTGTGGAGATTCACTTTTGGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240
Db	181	TGTGCTGTGTGGAGATTCACTTTTGGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240
Qy	241	CTGGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG	300
Db	241	CTGGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG	300
Qy	301	CCTCTCCAGGGCCCCAGCCTGGGCCACACCTTGCTTACAGGGCACTCTCAGATGCCCATAC	360
Db	301	CCTCTCCAGGGCCCCAGCCTGGGCCACACCTTGCTTACAGGGCACTCTCAGATGCCCATAC	360
Qy	361	CATAGTTTCTGTCTAGTGGACCGT	385
Db	361	CATAGTTTCTGTCTAGTGGACCGT	385

## RESULT 14

US-11-234-786-67 ; Sequence 67, Application US/11234786  
; Publication No. US20060024301A1

```

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-234-786-67

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Query Match 100.0%; Score 385; DB 16; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACTACACACTCCACTCCACTGCCCCTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA	60
Db	1	ACTACACACTCCACTGCCCCTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA	60
Qy	61	GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCACGACACATCAGGCTCTGAGAGTTC	120
Db	61	GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCACGACACATCAGGCTCTGAGAGTTC	120
Qy	121	CCCTTTTAAAAAGGGGACTTGCCTTTAAAAAGAGAGTCTAGCCACGATTGTGTAGAGCAGC	180
Db	121	CCCTTTTAAAAAGGGGACTTGCCTTTAAAAAGAGAGTCTAGCCACGATTGTGTAGAGCAGC	180
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCCTCTGAGACCGTGATCTTTAGAGG	240
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCCTCTGAGACCGTGATCTTTAGAGG	240
Qy	241	CTGGCGAGTCTTGCACATGAGATGGGGCTGTGCTGATCTCAGCACTCCTTAGTCTGCTTG	300

Db 241 CTGGCAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
Qy 301 CCTCTCCAGAGCCCCAGCCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360  
Db 301 CCTCTCCAGAGCCCCAGCCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360  
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 15

US-10-294-025-1036  
; Sequence 1036, Application US/10294025  
; Publication No. US20030185830A1  
; GENERAL INFORMATION:  
; APPLICANT: Stolk, John A.  
; APPLICANT: Kalos, Michael D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C29  
; CURRENT APPLICATION NUMBER: US/10/294,025  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 1038  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1036  
; LENGTH: 3710  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-294-025-1036

Query Match 99.2%; Score 381.8; DB 7; Length 3710;  
Best Local Similarity 99.5%; Pred. No. 8.4e-125;  
Matches 383; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 60  
Db 2282 ACCACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACACTTTAGGAATGCTGA 2341  
Qy 61 GGTGGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
Db 2342 GGTGAGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 2401  
Qy 121 CCCTTTTAAAAAGGGGACTTGCTTTAAAAAGAAAGTCTAGCCACGATTTGTGAGAGCAGC 180  
Db 2402 CCCTTTTAAAAAGGGGACTTGCTTTAAAAAGAAAGTCTAGCCACGATTTGTGAGAGCAGC 2461  
Qy 181 TGTGCTGTGCTGGAGATTACATTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240  
Db 2462 TGTGCTGTGCTGGAGATTACATTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 2521  
Qy 241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300  
Db 2522 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 2581  
Qy 301 CCTCTCCAGAGCCCCAGCCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360  
Db 2582 CCTCTCCAGAGCCCCAGCCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 2641  
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
Db 2642 CATAGTTTCTGTGCTAGTGGACCGT 2666

Search completed: December 31, 2006, 13:56:03  
Job time : 615.045 secs



Qy	1	ACTACACACACTCCACTTGTGCCCTTGTGAGACACTTTGTGCCAGACACTTTTAGGAATGCTGA	60
Db	1	ACTACACACACTCCACTTGTGCCCTTGTGAGACACTTTGTGCCAGACACTTTAGGAATGCTGA	60
Qy	61	GGTCGACCGACCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC	120
Db	61	GGTCGACCGACCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC	120
Qy	121	CCCTTTTAAAAAGGGGACTTCTCTTAAAAAAGAAGTCTAGCCACGATTTGTAGAGCAGC	180
Db	121	CCCTTTTAAAAAAGGGGACTTCTCTTAAAAAAGAAGTCTAGCCACGATTTGTAGAGCAGC	180
Qy	181	TGTGCTGTGCTGGAGATTACATTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG	240
Db	181	TGTGCTGTGCTGGAGATTACATTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG	240
Qy	241	CTGGGGCAGTCTTGCAATGAGATGGGGCTTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG	300
Db	241	CTGGGGCAGTCTTGCAATGAGATGGGGCTTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG	300
Qy	301	CCTCTCCCAAGGGCCCCAGCGCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC	360
Db	301	CCTCTCCCAAGGGCCCCAGCGCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC	360
Qy	361	CATAGTTTCTGTGCTAGTGGACCGT	385
Db	361	CATAGTTTCTGTGCTAGTGGACCGT	385

## RESULT 2

US-09-030-607-67  
; Sequence 67, Application US/09030607  
; Patent No. 6262245  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,607  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 385 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-09-030-607-67

Query Match	100.0%;	Score 385;	DB 3;	Length 385;
Best Local Similarity	100.0%;	Pred. No. 5.9e-124;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ACTACACACACTCCACTTGGCCCTTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA	60	
Db	1	ACTACACACACTCCACTTGGCCCTTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA	60	
Qy	61	GGTCGGACCAAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTC	120	
Db	61	GGTCGGACCAAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTC	120	
Qy	121	CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACAGATTGTTAGACGACG	180	
Db	121	CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACAGATTGTTAGACGACG	180	
Qy	181	TGTGCTGTGCTGGAGATTTCATTTTTCAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG	240	
Db	181	TGTGCTGTGCTGGAGATTTCATTTTTCAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG	240	
Qy	241	CTGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG	300	
Db	241	CTGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG	300	
Qy	301	CCCTCCCGGGCCCGAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC	360	
Db	301	CCCTCCCGGGCCCGAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC	360	
Qy	361	CATAGTTTCTGTCTAGTGGACCGT	385	
Db	361	CATAGTTTCTGTCTAGTGGACCGT	385	

### RESULT 3

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US-09-439-313-67
; Sequence 67, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGACACTTTTAGGAATGCTGA 60
      |||
Db      1  ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGACACTTTTAGGAATGCTGA 60

Qy      61  GGTGGGACCGACCATCTCATGTGCAAGATTGCCAGCAGACATCATGCTCAGAGTTC 120
      |||
Db      61  GGTGGGACCGACCATCTCATGTGCAAGATTGCCAGCAGACATCATGCTCAGAGTTC 120

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QY 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCAGATTGTTGTTAGAGCAGC 180  
Db 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCAGATTGTTGTTAGAGCAGC 180  
QY 181 TGTGCTGTGCTGAGAGTCACTTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240  
Db 181 TGTGCTGTGCTGAGAGTCACTTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGAGTCTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGCTTG 300  
Db 241 CTGGGAGTCTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGCCCCAGCTGGCCACACCTGCTTACAGGGCCTCTCAGATGCCATAC 360  
Db 301 CCTCTCCAGGCCCCAGCTGGCCACACCTGCTTACAGGGCCTCTCAGATGCCATAC 360  
QY 361 CATAGTTTCTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGCTAGTGGACCGT 385

## RESULT 4

US-09-352-616A-67  
; Sequence 67, Application US/09352616A  
; Patent No. 6395278  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Xu, Jiaangchun  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.427C8  
; CURRENT FILING DATE: 1999-07-13  
; NUMBER OF SEQ ID NOS: 472  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-352-616A-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60  
Db 1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60  
QY 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC 120  
Db 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC 120  
QY 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCAGATTGTTGTTAGAGCAGC 180  
Db 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCAGATTGTTGTTAGAGCAGC 180  
QY 181 TGTGCTGTGCTGAGAGTCACTTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240  
Db 181 TGTGCTGTGCTGAGAGTCACTTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGAGTCTTCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGCTTG 300  
Db 241 CTGGGAGTCTTCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGCCCCAGCTGGCCACACCTGCTTACAGGGCCTCTCAGATGCCATAC 360  
Db 301 CCTCTCCAGGCCCCAGCTGGCCACACCTGCTTACAGGGCCTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGCTAGTGGACCGT 385

## RESULT 5

US-09-232-149A-67  
; Sequence 67, Application US/09232149A  
; Patent No. 6465611  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiaangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; FILE REFERENCE: 210121.427C6  
; CURRENT APPLICATION NUMBER: US/09/232,149A  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-232-149A-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60  
Db 1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTGTCCAGCACTTTTAGGAATGCTGA 60  
QY 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC 120  
Db 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC 120  
QY 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCAGATTGTTGTTAGAGCAGC 180  
Db 121 CCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCAGATTGTTGTTAGAGCAGC 180  
QY 181 TGTGCTGTGCTGAGAGTCACTTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240  
Db 181 TGTGCTGTGCTGAGAGTCACTTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGAGTCTTCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGCTTG 300  
Db 241 CTGGGAGTCTTCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGCCCCAGCTGGCCACACCTGCTTACAGGGCCTCTCAGATGCCATAC 360  
Db 301 CCTCTCCAGGCCCCAGCTGGCCACACCTGCTTACAGGGCCTCTCAGATGCCATAC 360  
QY 361 CATAGTTTCTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGCTAGTGGACCGT 385

## RESULT 6

US-09-159-812-67  
; Sequence 67, Application US/09159812A  
; Patent No. 6613872  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiaangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF  
; FILE REFERENCE: 210121.428C5  
; CURRENT APPLICATION NUMBER: US/09/159,812A  
; CURRENT FILING DATE: 1998-09-23  
; NUMBER OF SEQ ID NOS: 306  
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 385; Conservative 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACATTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACATTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120
Qy 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCAGATTTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCAGATTTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240
Qy 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGSCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGSCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 7
US-09-636-215-67
; Sequence 67, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 385; Conservative 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACATTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACATTTGTCCAGCAGCACTTTAGGAATGCTGA 60
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCAGAGTTTC 120
Qy 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCAGATTTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAAGGGGACTTGTCTTAAAAAAGAGTCTAGCCAGATTTGTGTAGAGCAGC 180
Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACTTTTGTAGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240
Qy 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Db 241 CTGGGCAAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGSCACTCTCAGATGCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGSCACTCTCAGATGCCATAC 360
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 8
US-09-685-166A-67
; Sequence 67, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 385; Conservative 0;
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QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
DB 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
QY 61 GGTGGACACGACACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTGTGAGAGTTC 120  
DB 61 GGTGGACACGACACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTGTGAGAGTTC 120  
QY 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180  
DB 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180  
QY 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240  
QY 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
DB 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 9

US-09-115-453-67  
; Sequence 67, Application US/09115453B  
; Patent No. 6657056  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
; TITLE OF INVENTION: METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.427C4  
; CURRENT APPLICATION NUMBER: US/09/115,453B  
; CURRENT FILING DATE: 1998-07-14  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-115-453-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
DB 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
QY 61 GGTGGACACGACACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTGTGAGAGTTC 120  
DB 61 GGTGGACACGACACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTGTGAGAGTTC 120  
QY 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180  
DB 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180  
QY 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240  
QY 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
DB 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
RESULT 10  
US-09-688-489-67  
; Sequence 67, Application US/09688489  
; Patent No. 6664377  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.427D2  
; CURRENT APPLICATION NUMBER: US/09/688,489  
; CURRENT FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-688-489-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
DB 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
QY 61 GGTGGACACGACACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTGTGAGAGTTC 120  
DB 61 GGTGGACACGACACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTGTGAGAGTTC 120  
QY 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180  
DB 121 CCTTTTAAAAAGGGGACTTGTCTAAAAAGAGTCTAGCCACGATTGTGTAGACAGC 180  
QY 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCATTTTGGAGAGTTCTCTCTGAGACCTGATCTTTTAGAGG 240  
QY 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
DB 241 CTGGGCACTTTCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 11

US-09-679-426-67  
; Sequence 67, Application US/09679426  
; Patent No. 6759515  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C20  
; CURRENT APPLICATION NUMBER: US/09/679,426  
; CURRENT FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 895  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-679-426-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCACGACACTTTAGGAATGCTGA 60  
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCACGACACTTTAGGAATGCTGA 60  
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCATCAGTCTGAGAGTTC 120  
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCATCAGTCTGAGAGTTC 120  
Qy 121 CCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCATGTTGAGAGG 180  
Db 121 CCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCATGTTGAGAGG 180  
Qy 181 TGTGCTGTGCGAGATTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
Db 181 TGTGCTGTGCGAGATTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
Qy 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
Db 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360  
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360  
Qy 361 CATAGTTTCTGTGCTAGTGACCGT 385  
Db 361 CATAGTTTCTGTGCTAGTGACCGT 385

RESULT 12  
US-09-759-143-67  
; Sequence 67, Application US/09759143  
; Patent No. 6800746  
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-759-143-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCACGACACTTTAGGAATGCTGA 60  
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCACGACACTTTAGGAATGCTGA 60  
Qy 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCATCAGTCTGAGAGTTC 120  
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACATCATCAGTCTGAGAGTTC 120  
Qy 121 CCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCATGTTGAGAGG 180  
Db 121 CCTTTTAAAAAAGGGGACTTGTCTTAAAGAGTCTAGCCACATCATGTTGAGAGG 180  
Qy 181 TGTGCTGTGCGAGATTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
Db 181 TGTGCTGTGCGAGATTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
Qy 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
Db 241 CTGGCAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360  
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360  
Qy 361 CATAGTTTCTGTGCTAGTGACCGT 385  
Db 361 CATAGTTTCTGTGCTAGTGACCGT 385

RESULT 13  
US-09-651-236-67  
; Sequence 67, Application US/09651236  
; Patent No. 6818751  
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.42718C18  
CURRENT APPLICATION NUMBER: US/09/651,236  
CURRENT FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 865  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 67  
LENGTH: 385  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-651-236-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
QY 61 GTGCGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120  
DB 61 GTGCGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120  
QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180  
DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180  
QY 181 TGTGCTGTGCTGAGATTCACTTTTTCAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGAGATTCACTTTTTCAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTCTAGTCTGCTTG 300  
DB 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTCTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACTTGTCTTACAGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACTTGTCTTACAGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTCTGTGCTAGTGACCGT 385  
DB 361 CATAGTTCTGTGCTAGTGACCGT 385

RESULT 14  
US-09-030-606-67  
Sequence 67, Application US/09030606  
Patent No. 6887660  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,606  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.428C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-030-606-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 5.9e-124;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
QY 61 GTGCGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120  
DB 61 GTGCGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTTC 120  
QY 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180  
DB 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGAGCAGC 180  
QY 181 TGTGCTGTGCTGAGATTCACTTTTTCAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGAGATTCACTTTTTCAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTCTAGTCTGCTTG 300  
DB 241 CTGGGAGCTTTGCAATGAGATGGGGTGGTCTGATCTCAGCACTCTCTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACTTGTCTTACAGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCTGGCCACACTTGTCTTACAGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTCTGTGCTAGTGACCGT 385  
DB 361 CATAGTTCTGTGCTAGTGACCGT 385

RESULT 15  
US-09-657-279-67  
Sequence 67, Application US/09657279  
Patent No. 6894146  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C19

; CURRENT APPLICATION NUMBER: US/09/657,279

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 877

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-657-279-67

Query Match 100.0%; Score 385; DB 3; Length 385;

Best Local Similarity 100.0%; Pred. No. 5.9e-124;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACACTCCACTTGGCCCTTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60

Db 1 ACTACACACACTCCACTTGGCCCTTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60

Qy 61 GGTCCGACACGACCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

Db 61 GGTCCGACACGACCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

Qy 121 CCTTTTAAAAAAGGGGACTTGCCTTAAAAAAGAGCTAGCCACGATTGTGTAGAGCAGC 180

Db 121 CCTTTTAAAAAAGGGGACTTGCCTTAAAAAAGAGCTAGCCACGATTGTGTAGAGCAGC 180

Qy 181 TGTGCTGTGCTGGAGATTTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

Db 181 TGTGCTGTGCTGGAGATTTCACATTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

Qy 241 CTGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

Db 241 CTGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

Qy 301 CCTCTCCAGGGCCCCAGCCTGGCCACACACTGCTTTACAGGGCACTCTCAGATGCCCATAC 360

Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACACTGCTTTACAGGGCACTCTCAGATGCCCATAC 360

Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385

Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

Search completed: December 31, 2006, 12:31:10

Job time : 90.8616 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:07:59 ; Search time 299.256 Seconds  
(without alignments)  
8969.963 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

Sequence: 1 actacacacactcactctgc.....tttctgtgtagggaccgt 385

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	385	100.0	385	2	AAV61287
3	385	100.0	385	3	AAA06307
4	385	100.0	385	3	ABS71212
5	385	100.0	385	4	AAH93423
6	385	100.0	385	4	AAH93423
7	385	100.0	385	4	AAH02488
8	385	100.0	385	4	AAH84737
9	385	100.0	385	4	AAH86939
10	385	100.0	385	5	ACA59324
11	385	100.0	385	5	AAH10066
12	385	100.0	385	6	ABL94887
13	385	100.0	385	6	ABH58596
14	385	100.0	385	8	ACC95051
15	385	100.0	385	10	ADB13517
16	385	100.0	385	10	ADG26933
17	385	100.0	385	15	AEF66214
18	381.8	99.2	3710	10	ADB14486

19	318.2	82.6	1177	11	ACN90108	Acn90108 Breast ca
20	307.2	79.8	3218	15	AEF66848	Aef66848 Human pro
21	307.2	79.8	3228	4	AAH93865	Aah93865 P704P cDN
22	307.2	79.8	3228	4	AAH64037	Aas64037 Human pro
23	307.2	79.8	3228	5	ACA59845	Acas9845 Prostate
24	307.2	79.8	3228	6	ABL95408	AbL95408 Human P70
25	307.2	79.8	3228	8	ACC95572	Acc95572 Prostate
26	307.2	79.8	3228	10	ADB14151	AdB14151 Human pro
27	307.2	79.8	3228	10	ADG26567	Adg26567 Human pro
28	288.2	74.9	620	4	AAH22944	Aal22944 Human bre
29	284.4	73.9	606	4	AAH18894	Aal18894 Human bre
30	259.8	67.5	656	11	ACN87074	Acn87074 Breast ca
31	239	62.1	713	11	ACN84137	Acn84137 Breast ca
32	237.2	61.6	831	5	ABV26126	Abv26126 Human pro
33	237.2	61.6	831	5	ABV27659	Abv27659 Human pro
34	237.2	61.6	831	5	ABV21835	Abv21835 Human pro
35	237.2	61.6	831	11	ACN90279	Acn90279 Breast ca
36	224.8	58.4	516	4	AAH14082	Aal14082 Human bre
37	200	51.9	875	11	ACN81332	Acn81332 Breast ca
38	175.4	45.6	383	4	AAH15514	Aal15514 Human bre
39	175.4	45.6	407	4	AAH24358	Aal24358 Human bre
40	175.4	45.6	897	11	ACN85503	Acn85503 Breast ca
41	175.4	45.6	899	11	ACN91316	Acn91316 Breast ca
42	173.8	45.1	435	4	AAH18756	Aal18756 Human bre
43	172	44.7	354	4	AAH20352	Aal20352 Human bre
44	172	44.7	361	4	AAH11453	Aal11453 Human bre
45	172	44.7	417	11	ACN81654	Acn81654 Breast ca

#### ALIGNMENTS

#### RESULT 1

AAV58544

ID AAV58544 standard; cDNA; 385 BP.

XX

AC AAV58544;

XX

DT 25-MAR-2003 (revised)

DT 08-DEC-1998 (first entry)

XX

DE Prostate tumour specific gene clone P80.

XX

KW Prostate tumour specific gene; human; prostate cancer; detection;

KW

therapy; ss.

XX

OS Homo sapiens.

XX

PN WO9837418-A2.

XX

PD 27-AUG-1998.

XX

PF 25-FEB-1998; 98WO-US003690.

XX

PR 25-FEB-1997; 97US-00806596.

PR

01-AUG-1997; 97US-00904809.

PR

09-FEB-1998; 98US-00020747.

XX

(CORI-) CORIXA CORP.

PI

Xu J, Dillon DC;

XX

WPI; 1998-480805/41.

XX

Novel human prostate specific tumour protein and fragments - useful for

PT

detecting and treating prostate cancers.

PS

Claim 1; Page 64; 141pp; English.

XX

This sequence represents a human prostate tumour specific gene, and can

be used in the method of the invention. The method is for detecting

prostate cancer comprises contacting a biological sample with an agent

able to bind an immunogenic portion of a prostate protein (such as





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XX (CORI-) CORIXA CORP.
XX Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein.
XX
XX Claim 50; Page 120; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
XX immunogenic portion of a prostate tumor protein (PTP). The polypeptides
XX and polynucleotides encoding them have cytostatic activity and can be
XX used in vaccines and in gene therapy. The polypeptides and
XX polynucleotides encoding them, antigen presenting cells which express the
XX polypeptides, antibodies against the polypeptides and vaccines comprising
XX them can be used for inhibiting the development of prostate cancer in a
XX patient. The polypeptides can be used to generate antibodies or anti-
XX idiotypic antibodies for passive immuno therapy. A portion of the
XX polynucleotides encoding the polypeptides can be used as a probe or to
XX modulate the expression of the polypeptides. AA06241 to AAA06691 and
XX AA082000 to AA082020 represent sequences used in the exemplification of
XX the present invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 385; DB 3; Length 385;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX
XX 61 GGTGGGACAGCCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCGAGAGTTC 120
XX 61 GGTGGGACAGCCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCGAGAGTTC 120
XX
XX 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX
XX 181 TGTGCTGTGCTGAGATTCATCTTTGAGAGAGTTCCTCTGAGAGCTGATCTTTAGAGG 240
XX 181 TGTGCTGTGCTGAGATTCATCTTTGAGAGAGTTCCTCTGAGAGCTGATCTTTAGAGG 240
XX
XX 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTCAGATGCCATAC 360
XX 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTCAGATGCCATAC 360
XX
XX 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX
XX 361 CATAGTTTCTGCTAGTGACCGT 385
XX 361 CATAGTTTCTGCTAGTGACCGT 385
XX
XX RESULT 4
XX ABS71212 standard; cdNA; 385 BP.
XX
XX AC ABS71212;
XX
XX 27-NOV-2002 (first entry)
XX
XX Human prostate tumour protein partial DNA sequence #67.
XX
XX Human; immunogenic; prostate protein; prostate tumour protein;
XX prostate cancer; cytostatic; vaccine; 86.
```

09/119,453

```
XX Homo sapiens.
XX US2002090372-A1.
XX 11-JUL-2002.
XX
XX 14-JUL-1998; 98US-00115453.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX (XUJU/) XU J.
XX (DILL/) DILLON D C.
XX
XX Xu J, Dillon DC;
XX WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein.
XX
XX Claim 12; Page 40; 101pp; English.
XX
XX The present invention relates to a new polypeptide comprising an
XX immunogenic portion of a prostate protein. The invention is useful for
XX inhibiting the development of prostate cancer in a patient. The invention
XX is also useful as markers for diagnosing prostate cancer and for
XX monitoring diseases progression in patients. The present nucleic acid
XX sequence represents a DNA sequence that is part of a gene encoding a
XX human prostate tumour protein
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 385; DB 3; Length 385;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCAGCTTTAGGAATGCTGA 60
XX
XX 61 GGTGGGACAGCCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCGAGAGTTC 120
XX 61 GGTGGGACAGCCAGCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCGAGAGTTC 120
XX
XX 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX 121 CCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTGTAGAGCAGC 180
XX
XX 181 TGTGCTGTGCTGAGATTCATCTTTGAGAGAGTTCCTCTGAGAGCTGATCTTTAGAGG 240
XX 181 TGTGCTGTGCTGAGATTCATCTTTGAGAGAGTTCCTCTGAGAGCTGATCTTTAGAGG 240
XX
XX 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTCAGATGCCATAC 300
XX 241 CTGGGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCAGCTCTTCAGATGCCATAC 300
XX
XX 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
XX
XX 361 CATAGTTTCTGCTAGTGACCGT 385
XX 361 CATAGTTTCTGCTAGTGACCGT 385
XX
XX RESULT 5
XX AAH93423
XX ID AAH93423 standard; cdNA; 385 BP.
XX
XX
```

```
AC AAH93423;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P80 (also P740P).
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytotatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425973/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
PS Claim 1; Page 250; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. (I)
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 385; DB 4; Length 385;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTGTCCAGACACTTTCAGATGCTGA 60
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTGTCCAGACACTTTCAGATGCTGA 60
QY 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
DB 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAAAGGGAGCTTCTTAAAAAGAGTCTAGCCACGATGTGTAGAGCAGC 180
DB 121 CCCTTTTAAAAAGGGAGCTTCTTAAAAAGAGTCTAGCCACGATGTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTCACATTTTGGAGAGATTCCTCTCAGACCTGATCTTAGAGG 240
DB 181 TGTGCTGTGCTGGAGATTCACATTTTGGAGAGATTCCTCTCAGACCTGATCTTAGAGG 240
QY 241 CTGGGCGAGTCTTGACATGAGATGGGCTGTGATCTGATCTCAGCACTCTTGTGCTTG 300
DB 241 CTGGGCGAGTCTTGACATGAGATGGGCTGTGATCTGATCTCAGCACTCTTGTGCTTG 300
QY 301 CCTCTCCAGGGCCCGAGCTGGCCACACTGCTTACAGGGCACTCTCAGATGCCCATAC 360
DB 301 CCTCTCCAGGGCCCGAGCTGGCCACACTGCTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385
XX
XX RESULT 6
XX AAS63515
XX ID AAS63515 standard; cDNA; 385 BP.
XX
XX AAS63515;
XX
XX 29-JAN-2002 (first entry)
XX
XX Human prostate cDNA sequence #67.
XX
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
XX Homo sapiens.
XX
XX WO200173032-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001WO-US009919.
XX
XX 27-MAR-2000; 2000US-00536857.
XX
XX 09-MAY-2000; 2000US-00568100.
XX
XX 12-MAY-2000; 2000US-00570737.
XX
XX 13-JUN-2000; 2000US-00593793.
XX
XX 27-JUN-2000; 2000US-00605783.
XX
XX 09-AUG-2000; 2000US-00636215.
XX
XX 29-AUG-2000; 2000US-00651236.
XX
XX 06-SEP-2000; 2000US-00657279.
XX
XX 02-OCT-2000; 2000US-00679426.
XX
XX 10-OCT-2000; 2000US-00685166.
XX
XX 09-NOV-2000; 2000US-00709729.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Claim 1; Page 252; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polynucleotide of the invention
XX
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 385; DB 4; Length 385;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACCTTTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACCTTTTAGGAATGCTGA 60  
QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCGGAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCGGAGCAGACATCAGGTCTGAGAGTTC 120  
QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTTAGAGCAGC 180  
DB 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTTAGAGCAGC 180  
QY 181 TGTGCTGTCTGGAGATTCACTTTTGGAGAGATTCTCTTGAGACCTGATCTTTAGAGG 240  
DB 181 TGTGCTGTCTGGAGATTCACTTTTGGAGAGATTCTCTTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300  
DB 241 CTGGGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360  
DB 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360  
QY 361 CATAGTTTCTGTCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTCTAGTGGACCGT 385

## RESULT 7

AAH02488  
ID AAH02488 standard; cDNA; 385 BP.  
XX  
AC AAH02488;  
XX  
DT 14-JUN-2001 (first entry)  
XX  
DE Prostate tumour antigen determined cDNA sequence for P80.

XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;  
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.  
XX

OS Homo sapiens.

XX WO200125272-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US027464.

XX 04-OCT-1999; 99US-0157455P.

XX (CORI-) CORIXA CORP.

XX Xu J, Skeiky YAW, Reed SG, Cheever MA;

XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the  
PT treatment and diagnosis of prostate cancer.

XX Claim 50; Page 141; 276pp; English.

XX The present invention describes an isolated polypeptide (I) comprising at  
CC least an immunogenic portion of a prostate tumour antigen protein or its  
CC variant. (I) have cytostatic activity and can be used in vaccine  
CC production. (II), prostate tumour antigen polynucleotides, an antigen  
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a  
CC pharmaceutical composition containing (I) are useful for inhibiting the  
CC development of cancer in a patient. Antibodies specific for prostate  
CC specific proteins and oligonucleotides that hybridize to a polynucleotide  
CC that encodes a prostate specific protein are useful for detecting the

CC presence or absence of a cancer or monitoring the progression the  
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,  
CC AAH74798 to AAH74821 and AAH74830 are sequences used in the  
CC exemplification of the present invention

XX SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 385; DB 4; Length 385;

Best Local Similarity 100.0%; Pred. No. 1.8e-117;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTTGTCCAGCACCTTTTAGGAATGCTGA 60

DB 1 ACTACACACTCCACTTGGCTTGTGAGACACTTTTGTCCAGCACCTTTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCGGAGCAGACATCAGGTCTGAGAGTTC 120

DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCGGAGCAGACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTTAGAGCAGC 180

DB 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTTAGAGCAGC 180

QY 181 TGTGCTGTCTGGAGATTCACTTTTGGAGAGATTCTCTTGAGACCTGATCTTTAGAGG 240

DB 181 TGTGCTGTCTGGAGATTCACTTTTGGAGAGATTCTCTTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300

DB 241 CTGGGAGTCTTGACATGAGATGGGCTGGTCTGATCTCAGCACTCTTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360

DB 301 CCTCTCCAGGGCCCGAGCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTCTAGTGGACCGT 385

DB 361 CATAGTTTCTGTCTAGTGGACCGT 385

## RESULT 8

AAH84737  
ID AAH84737 standard; cDNA; 385 BP.

XX AAH84737;

XX 25-SEP-2001 (first entry)

XX Human prostate-specific cDNA sequence P80.

XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

KW chromosome 22q11.2; prostate-specific protein; chromosome 1;

KW prostate specific antigen; PSA; ss.

XX Homo sapiens.

XX WO200134802-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US030904.

XX 12-NOV-1999; 99US-00439313.

XX 18-NOV-1999; 99US-00443686.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;

XX WPI; 2001-308785/32.

XX Isolated polypeptide comprising at least an immunogenic portion of a

PT prostate-specific protein, useful in the diagnosis and therapy of  
PT prostate cancer.  
XX Claim 31; Page 150; 325pp; English.  
XX The present invention describes an isolated polypeptide (P1) comprising  
CC at least an immunogenic portion of a prostate-specific protein, or its  
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and  
CC (N1) have cytostatic activity and can be used in vaccine production. The  
CC polypeptides, nucleic acids and antibodies from the present invention are  
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific  
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic  
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.  
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.  
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide  
CC and polypeptide sequences used in the exemplification of the present  
CC invention  
XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 385; DB 4; Length 385;  
Best Local Similarity 100.0%; Pred. No. 1.8e-117;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACTCCACTTCCCTTGTGAGACACATTTGTCAGGACCTTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTCCCTTGTGAGACACATTTGTCAGGACCTTTAGGAATGCTGA 60  
QY 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
QY 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180  
DB 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCAGCATTGTGTAGAGCAGC 180  
QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCCTCTGAGACCTTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCCTCTGAGACCTTGATCTTTAGAGG 240  
QY 241 CTGGGAGCTTTGCAATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
DB 241 CTGGGAGCTTTGCAATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTTCTGCTAGTGAGCCGT 385  
DB 361 CATAGTTTCTGCTAGTGAGCCGT 385  
RESULT 9  
AAF86939  
ID AAF86939 standard; cDNA; 385 BP.  
XX AAF86939;  
AC AAF86939;  
XX  
DT 06-JUL-2001 (first entry)  
XX  
DE Human P704P inventive antigen coding sequence SEQ ID NO: 334.  
XX  
KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;  
KW chromosome 11p13; zinc finger transcription factor; ss.  
XX Homo sapiens.  
XX  
XX WO200125273-A2.  
XX  
PD 12-APR-2001.  
XX  
PF 04-OCT-2000; 2000WO-US027465.

XX 04-OCT-1999; 99US-0157459P.  
XX (CORI-) CORIXA CORP.  
XX Skeiky YAW, Xu J, Cheever MA, Reed SG;  
XX WPI; 2001-328324/34.  
XX Polypeptide comprising part of the Wilm's Tumor gene product sequence is  
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
PT and cancer associated with WT1.  
XX Disclosure; Page 213-214; 228pp; English.  
XX The present invention describes compositions comprising peptides derived  
CC from the Wilm's tumour protein WT1 and methods for their use in treating  
CC malignant diseases. Peptides derived from both the murine and human WT1  
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
CC and the protein was shown to be a zinc finger transcription factor. The  
CC immunogenic peptides of the invention are particularly useful in the  
CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
CC a coding sequence used in the exemplification of the invention  
XX  
SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;  
Query Match 100.0%; Score 385; DB 4; Length 385;  
Best Local Similarity 100.0%; Pred. No. 1.8e-117;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACTCCACTTCCCTTGTGAGACACATTTGTCAGGACCTTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTCCCTTGTGAGACACATTTGTCAGGACCTTTAGGAATGCTGA 60  
QY 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGAGCCAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
QY 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCACGATTGTGTAGAGCAGC 180  
DB 121 CCTTTTAAAAAGGGGACTTGCCTTAAAAAGAAAGTCTAGCCAGCATTGTGTAGAGCAGC 180  
QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCCTCTGAGACCTTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCCTCTGAGACCTTGATCTTTAGAGG 240  
QY 241 CTGGGAGCTTTGCAATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
DB 241 CTGGGAGCTTTGCAATGAGATGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTTCTGCTAGTGAGCCGT 385  
DB 361 CATAGTTTCTGCTAGTGAGCCGT 385  
RESULT 10  
ACA59324  
ID ACA59324 standard; cDNA; 385 BP.  
XX ACA59324;  
AC ACA59324;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Prostate cancer therapy associated cDNA #67.  
XX  
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;  
KW immunogen; cancer; prostate specific antigen; PSA;  
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;  
KW PSMA; gene; ss.

```
XX OS Homo sapiens.
XX US2002192763-A1.
XX PD 19-DEC-2002.
XX
XX PF 29-JUN-2001; 2001US-00895793.
XX PR 04-OCT-1999; 99US-0157455P.
XX PR 04-OCT-2000; 2000US-00679272.
XX PR 28-MAR-2001; 2001US-00822827.
XX
XX PA (XUJJ/) XU J.
XX PA (DILL/) DILLON D C.
XX PA (MITC/) MITCHAM J L.
XX PA (HARL/) HARLOCKER S L.
XX PA (JIAN/) JIANG Y.
XX PA (KALO/) KALOS M D.
XX PA (FANG/) FANGER G R.
XX PA (RETT/) RETTER M W.
XX PA (STOL/) STOLK J A.
XX PA (DAYC/) DAY C H.
XX PA (VEDV/) VEDVICK T S.
XX PA (CART/) CARTER D.
XX PA (LISX/) LI S X.
XX PA (WANG/) WANG A.
XX PA (SKEI/) SKEIKY Y A W.
XX PA (HEPL/) HEPLER W T.
XX PA (HEND/) HENDERSON R A.
XX PA (HURA/) HURAL J.
XX PA (MCNE/) MCNEILL P D.
XX PA (HOUG/) HOUGHTON R L.
XX PA (DBAS/) Y DE BASSOLS C V.
XX PA (FOYT/) FOY T M.
XX
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
XX PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM,
XX
XX DR WPI; 2001-245062/25.
XX
XX PT Prostate specific protein and its encoding polynucleotide, useful for the
XX PT treatment and diagnosis of prostate cancer.
XX
XX PS Example 3; SEQ ID NO 67; 85pp; English.
XX
XX CC The invention describes a fusion protein comprising at least one amino
XX CC acid sequence of immunogenic portions of any of the 3 sequences not
XX CC defined in the specification, or sequences having at least 70 or 90 %
XX CC sequence identity to any one of the 35 sequences defined in the USPTO web
XX CC site, which is encoded by any of the 4 nucleotide sequences not defined
XX CC in the specification. The fusion protein, composition and methods are
XX CC useful for diagnosing, preventing and/or treating cancer, particularly
XX CC prostate cancer. The proteins are useful as markers to indicate the
XX CC presence or absence of cancer. This sequence represents a prostate cancer
XX CC therapy associated cDNA. Note: The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from the US patent office at
XX CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
XX SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 385; DB 5; Length 385;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACTTTAGGAATCTGA 60
XX DB 1 ACTACACACTCCACTTGGCTTGTGAGACACTTGTCCAGCACTTTAGGAATCTGA 60
XX
XX QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTCTGAGAGTTC 120
```

```
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGCTCTGAGAGTTC 120
QY 121 CCCTTTTAAAAAAGGGGACTTCTCTTAAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180
Db 121 CCCTTTTAAAAAAGGGGACTTCTCTTAAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTCACATTTTGGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTCACATTTTGGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGACATCTCCTTAGTCTGCTTG 300
Db 241 CTGGGCGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGACATCTCCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGCCCCAGCCTCTGCGCCACACCTCTCTTACAGGGCAGCTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTCTGCGCCACACCTCTCTTACAGGGCAGCTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

```

RESULT 11  
AAS10066  
ID AAS10066 standard; cDNA; 385 BP.  
AC AAS10066;  
XX  
XX 24-OCT-2001 (first entry)  
XX Human prostate tumour cDNA P86 #4.  
XX Human; prostate tumour protein; prostate cancer; ss.  
XX Homo sapiens.  
XX US6262245-B1.  
XX 17-JUL-2001.  
XX 25-FEB-1998; 98US-00030607.  
XX 25-FEB-1997; 97US-00806099.  
XX 01-AUG-1997; 97US-00904804.  
XX 09-FEB-1998; 98US-00020956.  
XX (CORI-) CORIXA CORP.  
XX Xu J, Dillon DC;  
XX WPI; 2001-440862/47.  
XX Novel polynucleotide encoding polypeptide comprising a portion of  
XX prostate tumor protein useful for inhibiting development of prostate  
XX cancer or for treating prostate cancer in a patient.  
XX Example 2; Col 81; 105pp; English.  
XX The sequence is a human prostate tumour cDNA which encodes a partial  
XX tumour protein. The DNA is useful for inhibiting the development of  
XX prostate cancer or for treating prostate cancer in a patient  
XX  
XX SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 385; DB 5; Length 385;  
XX Best Local Similarity 100.0%; Pred. No. 1.8e-117;  
XX Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX

09/030, 687

```
QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGACACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTTAAAGGGGACTTGTCTTAAAGAGAGCTAGCCAGATTGTGTAGAGCAGC 180
Db 121 CCCTTTTAAAGGGGACTTGTCTTAAAGAGAGCTAGCCAGATTGTGTAGAGCAGC 180
QY 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGAGTTCCTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGAGCTTTGTCATGACATGAGATGGGGTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
Db 241 CTGGGAGCTTTGTCATGACATGAGATGGGGTGGTCTGATCTCAGCACTCCCTTAGTCTGCTTG 300
QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCAGCTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
```

## RESULT 12

ABL94887

ID ABL94887 standard; cDNA; 385 BP.

XX ABL94887;

XX

19-JUL-2002 (first entry)

Human P80 cDNA sequence SEQ ID NO 67.

Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;  
gene therapy; gene; ss.

Homo sapiens.

US2002022248-A1.

21-FEB-2002.

12-JAN-2001; 2001US-00759143.

25-FEB-1997; 97US-00806099.

01-AUG-1997; 97US-00904804.

10-FEB-1998; 98US-00020956.

25-FEB-1998; 98US-00030607.

14-JUL-1998; 98US-00115453.

23-SEP-1998; 98US-00159812.

15-JAN-1999; 99US-00232149.

09-APR-1999; 99US-00288946.

13-JUL-1999; 99US-00352616.

12-NOV-1999; 99US-00439313.

18-NOV-1999; 99US-00443686.

14-JAN-2000; 2000US-00483672.

27-MAR-2000; 2000US-00536857.

09-MAY-2000; 2000US-00568100.

12-MAY-2000; 2000US-00570737.

13-JUN-2000; 2000US-00593793.

27-JUN-2000; 2000US-00605783.

10-AUG-2000; 2000US-00636215.

29-AUG-2000; 2000US-00651236.

06-SEP-2000; 2000US-00657279.

02-OCT-2000; 2000US-00679426.

10-OCT-2000; 2000US-00685166.

(XUJ/) XU J.

(DILL/) DILLON D C.

(MITC/) MITCHAM J L.

```
PA (HAR/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
```

New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.

Claim 1; SEQ ID NO 67; 87pp; English.

The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention

Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 385; DB 6; Length 385;  
Best Local Similarity 100.0%; Pred. No. 1.8e-117;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACATCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60

Db 1 ACTACACACATCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60

QY 61 GGTGGACCCACATCTCATGTGCAAGATTGCCAGACACATCAGGTCTGAGAGTTC 120

Db 61 GGTGGACCCACATCTCATGTGCAAGATTGCCAGACACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180

Db 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCAGATTGTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

Db 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGGCACTCTTGACATGAGATGGGCTGCTGTGATCTCAGCACTCCTTAGTCTGCTTG 300

Db 241 CTGGGCACTCTTGACATGAGATGGGCTGCTGTGATCTCAGCACTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360

Db 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTTACAGGGCAGCTCTCAGATGCCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385

Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 13

ABS58596

ID ABS58596 standard; cDNA; 385 BP.

XX ABS58596;

XX

AC ABS58596;

XX

DT 05-NOV-2002 (first entry)  
 XX Prostate tumour cDNA #67.  
 DE Human; prostate tumour; immunotherapy; prostate cancer; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX US2002081580-A1.  
 XX 27-JUN-2002.  
 PD  
 XX 25-FEB-1998; 98US-00030606.  
 PF  
 XX 25-FEB-1997; 97US-00806596.  
 PR 01-AUG-1997; 97US-00904809.  
 PR 09-FEB-1998; 98US-00020747.  
 XX  
 PA (XUJJ/) XU J.  
 PA (DILL/) DILLON D C.  
 XX  
 XX Xu J, Dillon DC;  
 PI  
 XX WPI; 2002-607662/65.  
 DR  
 XX  
 XX Detecting prostate cancer comprises contacting a sample with an agent  
 PT capable of binding to a polypeptide with an immunogenic portion of a  
 PT prostate protein, oligonucleotide primers or a probe specific for DNA  
 PT encoding the polypeptide.  
 XX  
 XX Claim 1; Page 42-43; 11pp; English.  
 PS  
 CC The invention relates to a method of detecting prostate cancer by  
 CC contacting a biological sample from a patient with: (a) a binding agent  
 CC that binds to a polypeptide having an immunogenic portion of a prostate  
 CC protein or its variant; (b) 2 oligonucleotide primers, where 1 of the  
 CC oligonucleotides is specific for a DNA encoding the polypeptide of (a);  
 CC or (c) an oligonucleotide probe specific for a DNA molecule encoding the  
 CC polypeptide of (a). The method and polypeptides are useful for  
 CC diagnosing, treating, particularly by immunotherapy, monitoring the  
 CC progression, and inhibiting the development of prostate cancer in a  
 CC patient. The polypeptides may be used to generate antibodies useful  
 CC for the diagnosis and monitoring of prostate cancer. AB58530-AB58746  
 CC represent human prostate tumour cDNA sequences of the invention  
 XX  
 XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 385; DB 6; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-117;  
 Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
 DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
 QY 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
 DB 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
 QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180  
 DB 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180  
 QY 181 TGTGCTGTGCTGAGAGTTCATCTTTTGTGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
 DB 181 TGTGCTGTGCTGAGAGTTCATCTTTTGTGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
 QY 241 CTGGGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
 DB 241 CTGGGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
 QY 301 CCTCTCCAGGGCCCCAGCCTTGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360

Db 301 CCTCTCCAGGGCCCCAGCCTTGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
 QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
 Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
 RESULT 14  
 ACC95051  
 ID ACC95051 standard; cDNA; 385 BP.  
 XX  
 AC ACC95051;  
 XX  
 XX 28-AUG-2003 (first entry)  
 DT  
 XX Prostate tumour specific cDNA sequence SEQ ID 67.  
 DE  
 XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;  
 KW immune response; prostate cancer; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200289747-A2.  
 PN  
 XX 14-NOV-2002.  
 PD  
 XX 09-MAY-2002; 2002WO-US014753.  
 PF  
 XX 09-MAY-2001; 2001US-00852911.  
 PR 29-JUN-2001; 2001US-00895814.  
 PR 10-DEC-2001; 2001US-00012896.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;  
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;  
 PI Deng T;  
 PI WPI; 2003-167130/16.  
 DR  
 XX New prostate-specific proteins and genes, useful in gene therapy,  
 PT particularly for stimulating an immune response in a patient, or treating  
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer  
 PT in a patient.  
 XX  
 XX Example 3; Page 317; 691pp; English.  
 PS  
 CC The present invention relates to novel prostate-specific proteins (PSP)  
 CC and their coding sequences. The PSPs and their coding sequences are  
 CC useful for stimulating an immune response in a patient, or for treating  
 CC prostate cancer in a patient and for determining, detecting or diagnosing  
 CC the presence of a cancer in a patient. The present sequence was used to  
 CC illustrate the invention  
 XX  
 XX Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 385; DB 8; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-117;  
 Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
 DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
 QY 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
 DB 61 GGTCCGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
 QY 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180  
 DB 121 CCCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTAGCCACGATTTGTAGAGCAGC 180

```
QY 181 TGTGCTGCTGGAGATTCACTTTTGAGAGAGTTCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGCTGGAGATTCACTTTTGAGAGAGTTCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCACTTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTGTAGTCTGCTTG 300
Db 241 CTGGGCACTTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTGTAGTCTGCTTG 300
QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 15
ADBI3517
ID ADBI3517 standard; cDNA; 385 BP.
AC ADBI3517;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific cDNA P80/P704P.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00588100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
(PCORI-) CORIXA CORP.
XX
```

```
PI Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX
XX New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
XX Example 3; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is one of the
CC disclosed human prostate specific cDNAs. Note: Except where otherwise
CC indicated, the sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPIO at seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
SQ Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 385; DB 10; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCCTTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
Db 1 ACTACACACTCCACTTGCCCTTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
QY 61 GGTGGACCCACCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
Db 61 GGTGGACCCACCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120
QY 121 CCCTTTAAAAAGGGGACTTGCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
Db 121 CCCTTTAAAAAGGGGACTTGCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
QY 181 TGTGCTGTCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240
Db 181 TGTGCTGTCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG 240
QY 241 CTGGGCACTTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTGTAGTCTGCTTG 300
Db 241 CTGGGCACTTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCTTGTAGTCTGCTTG 300
QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360
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Db 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360  
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

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Job time : 300.256 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)  
9932.518 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

Sequence: 1 actacacacactccacttgc.....ttctgtgctagtggacogt 385

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb env.\*

2: gb pat.\*

3: gb ph.\*

4: gb pl.\*

5: gb pr.\*

6: gb ro.\*

7: gb sts.\*

8: gb sy.\*

9: gb un.\*

10: gb vi.\*

11: gb ov.\*

12: gb htg.\*

13: gb in.\*

14: gb om.\*

15: gb ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	100.0	385	2	BD070216
2	385	100.0	385	2	BD241980
3	385	100.0	385	2	AR237163
4	385	100.0	385	2	AR278187
5	385	100.0	385	2	AR366883
6	385	100.0	385	2	AR370779
7	385	100.0	385	2	AR392284
8	385	100.0	385	2	AR399919
9	385	100.0	385	2	AR405186
10	385	100.0	385	2	AR439390
11	385	100.0	385	2	AR563566
12	385	100.0	385	2	AR588552
13	385	100.0	385	2	AR605372
14	385	100.0	385	2	AR652986
15	385	100.0	385	2	AR656711
16	385	100.0	385	2	AR716618
17	385	100.0	385	2	AX106196
18	385	100.0	385	2	AX106286

19	385	100.0	385	2	AX140577	Sequence	
20	385	100.0	385	2	AX200437	Sequence	
21	385	100.0	385	2	AX267093	Sequence	
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C	24	373.4	97.0	5	CNS07EG2	Human chr	
C	25	371.8	96.6	5	CNS07EFD	Human chr	
C	26	371.8	96.6	5	CNS08CCG	Human chr	
C	27	370.2	96.2	5	AK125839	Homo sapi	
C	28	355.6	92.4	12	AC080181	Homo sapi	
C	29	351.4	91.3	12	AC124149	Pan trogl	
C	30	351	91.2	800	7	BV575629	Pan trogl
C	31	351	91.2	172816	5	AC123981	Pan trogl
C	32	349.8	90.9	751	7	BV589115	Pan trogl
C	33	349.8	90.9	232525	5	AC127023	Pan trogl
C	34	348.2	90.4	182216	12	AC182114	Pan trogl
C	35	319.8	83.1	178029	5	AC093838	Homo sapi
C	36	316.8	82.3	196097	5	AC122175	Pan trogl
C	37	315.2	81.9	176691	12	AC182395	Pan trogl
C	38	313.6	81.5	132753	5	AC131180	Homo sapi
C	39	313.6	81.5	184706	5	AC120781	Pan trogl
C	40	313.4	81.4	151820	12	AC140494	Homo sapi
C	41	312	81.0	165411	5	AC018865	Homo sapi
C	42	312	81.0	195514	5	AC018804	Homo sapi
C	43	312	81.0	241178	12	AC120839	Pan trogl
C	44	310.6	80.7	171176	5	AC119751	Homo sapi
C	45	310.4	80.6	168824	5	AC132479	Homo sapi

# ALIGNMENTS

RESULT 1	BD070216	385 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD070216	385 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Compounds for immunodiagnosis of prostate cancer and methods for their use.				
ACCESSION	BD070216				
VERSION	BD070216.1	GI:22615819			
KEYWORDS	JP 2001513886-A/67.				
SOURCE	JP 2001513886-A/67.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 385)				
AUTHORS	Xu,J. and Dillon,D.C.				
TITLE	Compounds for immunodiagnosis of prostate cancer and methods for their use				
JOURNAL	Patent: JP 2001513886-A 67 04-SEP-2001;				
COMMENT	CORIXA CORP				
OS	Homo sapiens (human)				
PN	JP 2001513886-A/67				
PD	04-SEP-2001				
PR	25-FEB-1998	JP 1998537008			
PR	25-FEB-1997	US 08/806596,01-AUG-1997	US	08/904809	PR
PI	09-FEB-1998	US 09/020747			
PC	JIANGCHON XU,DAVIN C DILLON				
PC	GO1N33/574,GO1N33/577,C07K16/30,A61K39/395,A61K47/48,C12Q1/68,GO1N33/543				
CC	Strandedness: Single;				
CC	Topology: Linear;				
CC	Compounds for immunodiagnosis of prostate cancer and methods for their use				
CC	Compounds for their use				
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FT	Location/Qualifiers				
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 CCTCTCCAGGGCCCGACCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360  
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Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

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LOCUS Compounds for immunotherapy and diagnosis of prostate cancer and  
DEFINITION methods for their use.  
ACCESSION BD241980  
VERSION BD241980.1 GI:33051750  
KEYWORDS JP 2002520054-A/67.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 385)  
Dillon,D.C., Harlocker,S.L., Yuqiu,J., Xu,J. and Mitcham,J.L.  
Compounds for immunotherapy and diagnosis of prostate cancer and  
methods for their use  
Patent: JP 2002520054-A 67 09-JUL-2002;  
CORIXA CORP  
OS Homo sapiens (human)  
PN JP 2002520054-A/67  
PF 09-JUL-2002  
PD 14-JUL-1999 JP 2000560247  
PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR  
23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR  
15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR  
09-APR-1999 US 09/288946  
PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI  
JIANGCHUN XU,  
PI JENNIFER LYNN MITCHAM  
PC C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,  
PC C12N5/10,  
PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,  
PC A61K37/02,  
PC C12N5/00  
CC Compounds for immunotherapy and diagnosis of prostate cancer  
and methods  
CC for their use  
FH Key Location/Qualifiers

FT source 1. 385  
FT Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 CTGGCAGCTTTGCACATGAGATGGGCTGTGATCTCAGCACTCCCTTAGTCTGCTTG 300  
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Qy 301 CCTCTCCAGGGCCCGACCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATAC 360  
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Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3  
AR237163 385 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 67 from patent US 6465611.  
DEFINITION AR237163  
ACCESSION AR237163  
VERSION AR237163.1 GI:27281821  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 385)  
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.  
TITLE Compounds for immunotherapy of prostate cancer and methods for  
their use  
JOURNAL Patent: US 6465611-A 67 15-OCT-2002;  
Corixa Corporation,Seattle, WA  
FEATURES  
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Db 61 GGTGGACCCACCATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
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Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 4  
LOCUS AR278187 385 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 67 from patent US 6512094.  
ACCESSION AR278187  
VERSION AR278187.1 GI:29712433  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 385)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6512094-A 67 28-JAN-2003;  
CORIXA Corporation; Seattle, WA  
FEATURES  
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Qy 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCTCTGAGACCTGATCTTTAGAGG 240  
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Qy 301 CCTCTCCAGGCCCCCAGCTGGCCACACCTGCTTACAGGCGACTCTCAGATGCCATAC 360  
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Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 5  
LOCUS AR366883 385 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 67 from patent US 6329505.  
ACCESSION AR366883  
VERSION AR366883.1 GI:34599858  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 385)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yuqiu, J., Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. and Day, C.H.  
TITLE Compositions and methods for therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6329505-A 67 11-DEC-2001;  
CORIXA Corporation; Seattle, WA  
FEATURES  
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Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 6  
LOCUS AR370779 385 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 67 from patent US 6395278.  
ACCESSION AR370779  
VERSION AR370779.1 GI:34607672  
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 385)
AUTHORS      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L. and Yugu,J.
TITLE        Prostate specific fusion protein compositions
JOURNAL      Patent: US 6395278-A 67 28-MAY-2002;
              Corixa Corporation; Seattle, WA
FEATURES     Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 67 from patent US 6620922.
ACCESSION  AR399919
VERSION     AR399919.1 GI:40142815
KEYWORDS    Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 385)
AUTHORS      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
              Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
              Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
              Hepler,W.T. and Henderson,R.A.
TITLE        Compositions and methods for the therapy and diagnosis of prostate
              cancer
JOURNAL      Patent: US 6620922-A 67 16-SEP-2003;
              Corixa Corporation; Seattle, WA
FEATURES     Location/Qualifiers
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RESULT 7
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LOCUS      AR392284
DEFINITION Sequence 67 from patent US 6613872.
ACCESSION  AR392284
VERSION     AR392284.1 GI:40116293
KEYWORDS    Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 385)
AUTHORS      Xu,J. and Dillon,D.C.
TITLE        Compounds for immunotherapy of prostate cancer and methods for
              their use
JOURNAL      Patent: US 6613872-A 67 02-SEP-2003;
              Corixa Corporation; Seattle, WA
FEATURES     Location/Qualifiers
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LOCUS      AR399919
DEFINITION Sequence 67 from patent US 6620922.
ACCESSION  AR399919
VERSION     AR399919.1 GI:40142815
KEYWORDS    Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 385)
AUTHORS      Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
              Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
              Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
              Hepler,W.T. and Henderson,R.A.
TITLE        Compositions and methods for the therapy and diagnosis of prostate
              cancer
JOURNAL      Patent: US 6620922-A 67 16-SEP-2003;
              Corixa Corporation; Seattle, WA
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Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 9  
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DEFINITION Sequence 67 from patent US 6630305.  
ACCESSION AR405186  
VERSION AR405186.1 GI:40154023  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 385)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6630305-A 67 07-OCT-2003;  
Corixa Corporation; Seattle, WA;  
WOX;

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DEFINITION Sequence 67 from patent US 6664377.  
ACCESSION AR439390  
VERSION AR439390.1 GI:42665299  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 385)  
AUTHORS Xu, J.

TITLE Compounds for immunotherapy of prostate cancer and methods for their use

JOURNAL Patent: US 6664377-A 67 16-DEC-2003;  
Corixa Corporation; Seattle, WA;  
WOX;

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Query Match 100.0%; Score 385; DB 2; Length 385;  
Best Local Similarity 100.0%; Pred. No. 3.8e-117;  
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DEFINITION Sequence 67 from patent US 6759515.  
ACCESSION AR563566  
VERSION AR563566.1 GI:53978617  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 385)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

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JOURNAL Patent: US 6759515-A 67 06-JUL-2004;
FEATURES Corixa Corporation; Seattle, WA
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QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
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DEFINITION Sequence 67 from patent US 6818751.
ACCESSION AR605372
VERSION AR605372.1 GI:56657036
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6818751-A 67 16-NOV-2004;
Corixa Corporation; Seattle, WA
FEATURES Location/Qualifiers
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DEFINITION Sequence 67 from patent US 6800746.
ACCESSION AR588552
VERSION AR588552.1 GI:56635449
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6800746-A 67 05-OCT-2004;
Corixa Corporation; Seattle, WA
FEATURES Location/Qualifiers
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ACCESSION AR652986  
VERSION AR652986.1 GI:67583223  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Xu, J. and Dillon, D. C.  
TITLE Compounds for immunodiagnosis of prostate cancer and methods for their use  
JOURNAL Patent: US 6887660-A 67 03-MAY-2005;  
FEATURES Corixa Corporation; Seattle, WA  
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DEFINITION Sequence 67 from patent US 6894146.  
ACCESSION AR656711  
VERSION AR656711.1 GI:67589779  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedwick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T., and Henderson, R. A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6894146-A 67 17-MAY-2005;  
FEATURES Corixa Corporation; Seattle, WA  
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Post-processing: Minimum Match 0%

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#### SUMMARIES

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#### ALIGNMENTS

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DB045159	sequence.						
DB045159	DB045159.1	GI:82061582					
EST.	Homo sapiens (human)						
Homo sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.							
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Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.							
Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes							
Genome Res. 16 (1), 55-65 (2006)							
16344560							
Contact: Takao Isogai							
FLJ Project (HRI Team)							
Helix Research Institute							
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan							
Tel: 81-438-52-3975							
Fax: 81-438-52-3986							
Email: flj-cdna@nifty.com							
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.							
Location/Qualifiers							
1..556							
/organism="Homo sapiens"							
/mol_type="mRNA"							

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/db_xref="taxon:9606"
/clone="TESTII2033322"
/tissue_type="testis"
/clone_lib="TESTI2"
/note="Vector: pME18SFL3"
```

## ORIGIN

```
Query Match      81.2%; Score 312.8; DB 9; Length 556;
Best Local Similarity 92.4%; Pred. No. 4.2e-83;
Matches 340; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

Qy 12 TCCACTTCCCTTGAGACACTTTGTCGCCAGCACTTTAGGAATGCTCAGGTGCGACAG 71
Db 189 TCTACTTGCCCTTGAGACACTTTATCCAGCACTTTAGGAATGCTCAGGTATACCA 248

Qy 72 CCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTCCCTTTTAAA 131
Db 249 CCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCCAGAGTTCTCTGTTTAAA 308

Qy 132 AAGGGGACTTGTCTTAA-AAAAGAAGCTAGCCACGATTTGTAGAGCAGCTGTGCTGTGC 190
Db 309 AAGGGGACTTGTCTTAAATAAAGAAGCTGTGGCCATGTTTGTGTAGAGCAGCTGTGCTGTGC 368

Qy 191 TGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGGCTGGGCGATC 250
Db 369 TGGGGGTTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTCTGAGAGGCTGGGCGATC 428

Qy 251 TTGCACATGAGATGGGGTGTGCTGATCTCAGCACTCTCTTGTGCTTGTGCTCTCCAG 310
Db 429 TTGCACATGAGATGGGGTGTGCTGATGGCAGCACTCTCTTGTGCTTGTGCTCTCCAT 488

Qy 311 GGGCCAGCTGGGCCACACTCTTACAGGGCAGCTCTCAGATGCCATACATAGTTTCT 370
Db 489 GGGCCAGCTGGGCCACACTCTTACAGGGCAGCTCTTACAGGGCAGCTCTTACAGGGCAGCTCTCC 548

Qy 371 GTGCTAGT 378
Db 549 GTGCTAGT 556
```

## RESULT 2

```
BQ068886/c
LOCUS      BQ068886      986 bp      mRNA      linear      EST 02-APR-2002
DEFINITION AGENCOURT_6740305 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802737
5', mRNA sequence.
ACCESSION  BQ068886
VERSION    BQ068886.1  GI:19897932
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
            1 (bases 1 to 986)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM2037 row: j column: 18
            High quality sequence stop: 751.
            Location/Qualifiers
            1..986
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
```

## FEATURES

source

```
/clone="IMAGE:5802737"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
```

## ORIGIN

```
Query Match      60.2%; Score 231.8; DB 3; Length 986;
Best Local Similarity 88.0%; Pred. No. 1.6e-58;
Matches 265; Conservative 0; Mismatches 32; Indels 4; Gaps 1;

Qy 11 CTCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTCCCTTTTAAA 70
Db 414 CTCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTCCCTTTTAAA 355

Qy 71 GCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTCCCTTTTAAA 130
Db 354 GCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTCCCTTTTAAA 295

Qy 131 AAAGGGGACTTGTCTTAAATAAAGAAGCTAGCCACGATTTGTGTAGAGCAGCTGTGCTGTGC 190
Db 294 AAAGGGGACTTGTCTTAAATAAAGAAGCTAGCCACGATTTGTGTAGAGCAGCTGTGCTGTGC 235

Qy 191 TGGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGGCTGGGCGATC 250
Db 234 CGGGGGTTCATCTTTTGAGAGAGTTCTCTCTGAGACCTGATCTCTCTCTCTCTCTCTCT 179

Qy 251 TTGCACATGAGATGGGGTGTGCTGATCTCAGCACTCTCTTGTGCTTGTGCTTGTGCTTGTGCT 310
Db 178 CTGCACATGAGATGGGGTGTGCTGATATCAGCACTCTCTTGTGCTTGTGCTTGTGCTTGTGCT 119

Qy 311 G 311
Db 118 G 118
```

## RESULT 3

```
CD251924
LOCUS      CD251924      861 bp      mRNA      linear      EST 22-MAY-2003
DEFINITION AGENCOURT_14204354 NIH_MGC_180 Homo sapiens cDNA clone
IMAGE:30383087 5', mRNA sequence.
ACCESSION  CD251924
VERSION    CD251924.1  GI:31012390
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
            1 (bases 1 to 861)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
```

Plate: NDAM446 row: f column: 24

High quality sequence stop: 701.

#### FEATURES

source

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1. .861
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30383087"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_180"
/notes="Organ: testis; Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
```

#### ORIGIN

```
Query Match 29.2%; Score 112.4; DB 5; Length 861;
Best Local Similarity 99.1%; Pred. No. 2e-22;
Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 272 TCTGATCTCAGCACTCTAGTCTGCTTCCAGGGCCCGCCAGCTGGCCACACCT 331
Db |||
560 TCTGATCTCAGCACTCTAGTCTGCTTCCAGGGCCCGCCAGCTGGCCACACCT 619
QY 332 GCTTACAGGCACTCTCAGATGCCATACATAGTTTCTGCTAGTGACCGT 385
Db |||
620 GCTTACAGGCACTCTCAGATGCCATACATAGTTTCTGCTAGTGACCGT 673
```

#### RESULT 4

```
DN920910 491 bp mRNA linear EST 20-OCT-2005
LOCUS MCF7RNA128p21TR Human MCF7 breast cancer cell line near full length
DEFINITION normalized library (MCF7 EST) Homo sapiens cDNA clone
MCF7 RNA L_28_p21, mRNA sequence.

ACCESSION DN920910.1 GI:77951595
VERSION DN920910.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 491)
Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Bajzarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
Jong,P., Pevzner,P. and Collins,C.
Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
tumor genome project
Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7067
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
Seq primer: SP6 5'-ATTAGTGACACTAGATAC-3'.
```

#### FEATURES

source

```
1. .491
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MCF7 RNA_L_28_p21"
/sex="female"
/cell_line="MCF7"
/clone_lib="Human MCF7 breast cancer cell line near full
length normalized library (MCF7 EST)"
/note="Vector: pAL17; This library was constructed from
```

#### ORIGIN

```
Query Match 29.0%; Score 111.8; DB 9; Length 491;
Best Local Similarity 90.2%; Pred. No. 2.7e-22;
Matches 119; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 254 CACATGAGATGGGGTGGTCTGATCTCAGCACTCTCTAGTCTGCTCTCCAGGGC 313
Db |||
353 CACATGAGATGGGGTGGTCTGATGCGCACTCTCTTANTCTGTTGGCTCTCCCATGG 412
QY 314 CCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCATACCATAGTTTCTGTG 373
Db |||
413 CCTAGCTGGCCACACATCTTACAGGCACTCTTAGATGCCACACTAGTCTGCGTG 472

QY 374 CTATGGGACCGT 385
Db |||
473 CTATGGGACCTGT 484
```

#### RESULT 5

```
BC063888 5483 bp mRNA linear HTC 09-DEC-2005
LOCUS Homo sapiens prostate-specific P704P mRNA, mRNA (cDNA clone
IMAGE:30389199), with apparent retained intron.
ACCESSION BC063888
VERSION BC063888.1 GI:39645658
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 5483)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Lequellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
Mckernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 5483)
```

#### REFERENCE

##### AUTHORS

NIH MGC Project  
Direct Submission  
Submitted (08-DEC-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILML)  
DNA Sequencing by: Genome Sequence Centre,

##### CONSRMT

##### TITLE

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
CONSRMT  
TITLE  
JOURNAL  
REMARK  
COMMENT

##### CONSRMT

##### TITLE

##### JOURNAL

##### REMARK

##### COMMENT

BC Cancer Agency, Vancouver, BC, Canada  
info@bcgsc.bc.ca  
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smalrus, Jeff Stott, Miranda Tsai, George Yang, Jacques Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 141 Row: 0 Column: 10  
This clone has the following problem: retained intron.

## FEATURES

source

1..5483  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30389199"  
/tissue\_type="Testis"  
/clone\_lib="NIH MGC\_180"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6.1"

## ORIGIN

Query Match 27.9%; Score 107.4; DB 6; Length 5483;  
Best Local Similarity 99.1%; Pred. No. 1.1e-20;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 277 TCTCAGCACTCTTAGTCTGCTTCCAGGCCCCAGCCCTGGCCACACCTGCTTA 336  
||  
Db 3936 TCCAGCACTCTTAGTCTGCTTCCAGGCCCCAGCCCTGGCCACACCTGCTTA 3995  
||  
Qy 337 CAGGCACTCTCAGATGCCATACATAGTTCTGCTAGTGGACCGT 385  
||||  
Db 3996 CAGGCACTCTCAGATGCCATACATAGTTCTGCTAGTGGACCGT 4044  
||||

## RESULT 6

HSMB09270/c HSM809270 6098 bp mRNA linear HTC 20-JAN-2005  
LOCUS Homo sapiens mRNA; cDNA DKFP686J0529 (from clone DKFP686J0529).  
DEFINITION  
ACCESSION BX649118  
VERSION BX649118.1 GI:34368290

KEYWORDS

SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS

Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.

CONSRMTM

The German cDNA Consortium

TITLE

Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764

JOURNAL

Neuberberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email [s.wiemann@dkfz-heidelberg.de](mailto:s.wiemann@dkfz-heidelberg.de); sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

COMMENT

This clone (DKFP686J0529) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFP686J0529>  
Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

## FEATURES

source

1..6098  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="RZPD:DKFP686J0529Q"  
/db\_xref="taxon:9606"  
/clone="DKFP686J0529"  
/tissue\_type="testis"  
/clone\_lib="686 (synonym: hlcc3). Vector pSport1\_sfi; host DH10B; sites SfiIA + SfiIB"  
/dev\_stage="adult"  
/note="putative transcript"

## ORIGIN

Query Match 26.4%; Score 101.8; DB 6; Length 6098;  
Best Local Similarity 93.8%; Pred. No. 5.4e-19;  
Matches 106; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 248 GTCTTGACATGAGATGGGCTGTGTGATCTCAGCACTCTTAGTCTGTGCTCTCC 307  
||||  
Db 5065 GTCTTGACATGAGATGGGCTGTGTGATCTCAGCCCTCCCTAGTCTGTGCTCTCC 5006  
||||

Qy 308 CAGGCCCCAGCCCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCATAC 360  
||||

Db 5005 CAGGACCCAGCCCTGGCCACACCTGCTTACAGGCACTCTCAGATGCCACAC 4953  
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## RESULT 7

DA554900

LOCUS

DA554900 HCHON2 Homo sapiens cDNA clone HCHON2005010 5', mRNA  
sequence.

ACCESSION

DA554900

VERSION

DA554900.1 GI:80884861

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 553)  
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

TITLE

Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative

PROMOTERS OF HUMAN GENES

Genome Res. 16 (1), 55-65 (2006)

JOURNAL

PUBMED

COMMENT

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: [flj-cdna@infocity.com](mailto:flj-cdna@infocity.com)

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

Location/Qualifiers

1..553

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HCHON2005010"

/cell\_type="chondrocytes (HC)"

/clone\_lib="HCHON2"

/note="Vector: pME18SFL3; primary culture, chondrocytes"

## ORIGIN

Query Match 26.2%; Score 100.8; DB 9; Length 553;  
 Best Local Similarity 90.0%; Pred. No. 5.8e-19;  
 Matches 108; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 240 GCTGGGAGCTTTCACATGAGATGGGGCTGGTCTGATCTCAGACATCCCTTAGTCTGCTT 299  
 |||||  
 DB 105 GCTGGGAGCTTTCACATGAGATGGGGCTGGTCTGATCTCAGACATCCCTTAGTCTGCTT 164  
 |||||  
 QY 300 GCTCTCTCCAGGGCCCGAGCTGGCCACACTGCTTACAGGGCACTCTCAGATGCCCATTA 359  
 |||||  
 DB 165 GCTCTCTCCAGGGCCCGAGCTGGCCACACTGCTTACAGGGCACTCTCAGATGCCCATTA 224  
 |||||

RESULT 8  
 BQ068886  
 LOCUS BQ068886 986 bp mRNA linear EST 02-APR-2002  
 DEFINITION AGENCOURT\_6740305 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:5802737  
 5', mRNA sequence.

ACCESSION BQ068886  
 VERSION BQ068886.1 GI:119897932  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 986)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: rgabs-r@mail.nih.gov  
 Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LCM2037 row: j column: 18  
 High quality sequence stop: 751.  
 Location/Qualifiers  
 1. .986  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5802737"  
 /tissue\_type="neuroblastoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_47"  
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAAGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## FEATURES

source

## ORIGIN

Query Match 24.7%; Score 95; DB 3; Length 986;  
 Best Local Similarity 65.1%; Pred. No. 3.8e-17;  
 Matches 157; Conservative 0; Mismatches 80; Indels 4; Gaps 1;

QY 51 GGAATGCTGAGGTGGGACCGACATCTCATGTGCAAGATTGCCAGCAGACATCAGGT .110  
 |||||  
 DB 141 GGAGTGTGATATCAGACACCGCCCATCTCATGTGCGAGGACTGCCAGCAGACATCAGGT 200  
 |||||  
 QY 111 CTGAGAGTTCCTCTTTTAAAAAGGGGACTTGTCTTAAAAAGAGTCTACGCCACAGTTGT 170  
 |||||  
 DB 201 CTCAGAGGAGAACTGTCTCAAAAGTGAACCCCGGCGACAGCATAGTGTCTTACACAAC 260  
 |||||

QY 171 GTAGACAGCTGTGCTGTGAGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGA 230  
 |||||  
 DB 261 ATGCCCAGGCTTCTTTTGGAGCAAGTCCCTTTTGAAGAGGGAACTCTGGGAACTGA 320  
 |||||  
 QY 231 TCTTTAGAGCTGGGAGCTTTCACATGAGATGGGGCTGGTCTGATCTCAGACATCCTT 290  
 |||||  
 DB 321 TCTCT-----GCTGGGAGTCTTTGAACATGAGATGGGGCTGATCTGAATTCCTA 376  
 |||||

QY 291 A 291  
 DB 377 A 377

RESULT 9  
 CD251853  
 LOCUS CD251853 873 bp mRNA linear EST 22-MAY-2003  
 DEFINITION AGENCOURT\_14206078 NIH\_MGC\_180 Homo sapiens cDNA clone  
 IMAGE:30383062 5', mRNA sequence.

ACCESSION CD251853  
 VERSION CD251853.1 GI:31012319  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 873)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-r@mail.nih.gov

CDNA Library Preparation: Invitrogen Corp  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
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 constructed by (Invitrogen). Note: this is a NIH\_MGC  
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## FEATURES

source

## ORIGIN

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 Matches 108; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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 DB 534 TCTGATCTCAGCACTCTTTAGTCTGCTTCCAGGGCCCCAGCTGGCCACCT 593  
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 QY 332 GTTACAGGGCACTCTCA-GATGCCCATACCATAGTTTCTGTGCTAGTGGCCGT 385  
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 DB 594 GCTTACAGGGCACTCTCAGGGTGGCCCATACCATAGTTTCCGGGCCAGGGGACCGT 648  
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was generated during the R&D process and may have higher chance of clone tracking errors.

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Sequencing: -21M13

## LIBRARY

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## FEATURES

source

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Best Local Similarity 74.2%; Pred. No. 7.2e-12;  
Matches 115; Conservative 0; Mismatches 31; Indels 9; Gaps 1;  
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DB 198 GCAAAATCTCTGGGGCCCCGCTGATCGCTACTTACAGTGCAGTCTCAGGTACCTGA 139  
QY 351 ATGCCCATACCATAGTTTCTGTCTAGTGGACCGT 385  
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## RESULT 13

AG094252/c

LOCUS

AG094252

DEFINITION

AG094252

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## RESULT 14

CR748036/c

LOCUS

CR748036

DEFINITION

CR748036

CR748036

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## RESULT 14

CR748036/c

LOCUS

CR748036

DEFINITION

CR748036

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## RESULT 14

CR748036/c

LOCUS

CR748036

DEFINITION

CR748036

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## RESULT 14

CR748036/c

LOCUS

CR748036

DEFINITION

CR748036

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VERSION AQ784117.1 GI:5691741  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 527)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and  
Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
PUBMED 10449764  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: http://www.htsec.washington.edu  
Plate: 3034 row: B column: 21  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 527.  
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Job time : 3091.06 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:22:01 ; Search time 613.045 Seconds  
(without alignments)  
7716.790 Million cell updates/sec

Title: US-09-232-880-67

Perfect score: 385

Sequence: 1 actacacacacccttcgtgc.....ttctgtgtagtgaccgt 385

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	100.0	385	3	US-09-759-143-67 Sequence 67, Appl
2	385	100.0	385	3	US-09-780-669-67 Sequence 67, Appl
3	385	100.0	385	3	US-09-030-606-67 Sequence 67, Appl
4	385	100.0	385	3	US-09-822-827-67 Sequence 67, Appl
5	385	100.0	385	3	US-09-115-453-67 Sequence 67, Appl
6	385	100.0	385	3	US-09-232-880-67 Sequence 67, Appl
7	385	100.0	385	3	US-09-895-793-67 Sequence 67, Appl
8	385	100.0	385	3	US-09-895-814-67 Sequence 67, Appl
9	385	100.0	385	6	US-10-012-896-67 Sequence 67, Appl
10	385	100.0	385	6	US-10-010-940-67 Sequence 67, Appl
11	385	100.0	385	7	US-10-144-678A-67 Sequence 67, Appl
12	385	100.0	385	7	US-10-294-025-67 Sequence 67, Appl
13	385	100.0	385	8	US-10-688-838-67 Sequence 67, Appl
14	385	100.0	385	16	US-11-234-786-67 Sequence 67, Appl
15	381.8	99.2	3710	7	US-10-294-025-1036 Sequence 1036, Appl
16	318.2	82.6	1177	6	US-10-198-846-11258 Sequence 11258, A
17	307.2	79.8	3218	16	US-11-234-786-701 Sequence 701, Appl

ALIGNMENTS

RESULT 1

US-09-759-143-67

; Sequence 67, Application US/09759143

; Patent No. US2002002248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapien

; US-09-759-143-67

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Best Local Similarity 100.0%; Pred. No. 2.2e-126;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
US-09-780-669-67  
; Sequence 67, Application US/09780669  
; Patent No. US20020051977A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C24  
; CURRENT APPLICATION NUMBER: US/09/780,669  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 943  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-780-669-67

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Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

RESULT 3  
US-09-030-606-67  
; Sequence 67, Application US/09030606  
; Patent No. US20020081580A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,606  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.428C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 385 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-09-030-606-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACTACACACATCTCCACTTGGCCCTCTGTGAGACACATTTGTGCCAGCACCTTTAGGAATGCTGA	60
Db	1	ACTACACACACTCCACTTGGCCCTTGTGAGACACATTTGTGCCAGCACCTTTAGGAATGCTGA	60
Qy	61	GGTCGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC	120
Db	61	GGTCGACACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTCAGAGTTTC	120
Qy	121	CCCTTTTAAAAAAGGGGACTTCGTTTAAAAAAGAAAGTCTTAGCCACGATGTGTAGAGCAGC	180
Db	121	CCCTTTTAAAAAAGGGGACTTCGTTTAAAAAAGAAAGTCTTAGCCACGATGTGTAGAGCAGC	180
Qy	181	TGTGCTGTGCTCGAGATTACATTTTGTGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240
Db	181	TGTGCTGTGCTCGAGATTACATTTTGTGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240
Qy	241	CTGGGCAGTCTTGCAATGAGATGGGGCTGTGTCATCTCAGACACTCCTTAGTCTGCTTG	300
Db	241	CTGGGCAGTCTTGCAATGAGATGGGGCTGTGTCATCTCAGACACTCCTTAGTCTGCTTG	300
Qy	301	CCTCTCCCGAGGGCCCCAGCGCTGGCCACACCTGCTTTACAGGCGACTCTCAGATGCCATAC	360
Db	301	CCTCTCCCGAGGGCCCCAGCGCTGGCCACACCTGCTTTACAGGCGACTCTCAGATGCCATAC	360
Qy	361	CATAGTTTCTGTGCTAGTGGACCGT	385
Db	361	CATAGTTTCTGTGCTAGTGGACCGT	385

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RESULT 4
US-09-822-827-67
; Sequence 67, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 392
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-67

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Query Match	100.0%	Score 385;	DB 3;	Length 385;
Best Local Similarity	100.0%;	Pred. No. 2.2e-126;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ACTACACACATCCACTTGCCTTGTGTGAGACACATTTGTCCAGCACATTTTAGAATGCTGA	60	
Db	1	ACTACACACATCCACTTGCCTTGTGTGAGACACATTTGTCCAGCACATTTTAGAATGCTGA	60	
Qy	61	GGTCGGACACGCCACATCTCATGTGCAAGATTGCCACAGACATCAGGTCGTGAGAGTTC	120	
Db	61	GGTCGGACACGCCACATCTCATGTGCAAGATTGCCACAGACATCAGGTCGTGAGAGTTC	120	
Qy	121	CCCTTTTAAAAAGGGGACTTGCTTTAAAAAGAAAGTCTAGCCACGATTTGTGTAGAGCAGC	180	
Db	121	CCCTTTTAAAAAGGGGACTTGCTTTAAAAAGAAAGTCTAGCCACGATTTGTGTAGAGCAGC	180	
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240	
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGTGAGAGAGTTCTCCTCTGAGACCTGATCTTTTAGAGG	240	
Qy	241	CTGGGCGAGTCTTGCACATGAGATGGGGCTGCTCTGATCTCAGCACTCCTTAACTGCTGCTTG	300	
Db	241	CTGGGCGAGTCTTGCACATGAGATGGGGCTGCTCTGATCTCAGCACTCCTTAACTGCTGCTTG	300	
Qy	301	CCTCTCCACGGGCCCCACGCTGGGCCACACCTGCTTTACAGGGGCATCTCAGATGCCCATAC	360	

Db	301	CCTCTCCAGGGCCCCAGCCCTGGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC	360
Qy	361	CATAGTTTCTGCTGCTAGTGGACCGT	385
Db	361	CATAGTTTCTGCTGCTAGTGGACCGT	385

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RESULT 5
US-09-115-453-67
; Sequence 67, Application US/09115453B
; Patent No. US2002090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115.453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-67

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Query Match	100.0%;	Score 385;	DB 3;	Length 385;	
Best Local Similarity	100.0%;	Pred. No. 2.2e-136;			
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	ACTACACACACTCCACTTGCCTTTGTGAGACACACTTTGTCCAGCAGCACTTTAGGAATGCTGA	60		
Db	1	ACTACACACACTCCACTTGCCTTTGTGAGACACACTTTGTCCAGCAGCACTTTAGGAATGCTGA	60		
Qy	61	GGTCGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGTCTGAGAGTTC	120		
Db	61	GGTCGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGTCTGAGAGTTC	120		
Qy	121	CCCTTTTAAAAAGGGGACCTTGCCTTTAAAAAGAGAGTCTAGCCACCATTGTGTAGAGCAGC	180		
Db	121	CCCTTTTAAAAAGGGGACCTTGCCTTTAAAAAGAGAGTCTAGCCACCATTGTGTAGAGCAGC	180		
Qy	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTTAGAGG	240		
Db	181	TGTGCTGTGCTGGAGATTCACTTTTGGAGAGATTCTCCTCTGAGACCTGATCTTTTAGAGG	240		
Qy	241	CTGGGCGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACCTCCTTAGTCTGCTTG	300		
Db	241	CTGGGCGAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACCTCCTTAGTCTGCTTG	300		
Qy	301	CCTCTCCAGGGCCCCAGCCTGGGCCACACCTTGTACAGGGGCACCTCTCAGATGCCCATAC	360		
Db	301	CCTCTCCAGGGCCCCAGCCTGGGCCACACCTTGTACAGGGGCACCTCTCAGATGCCCATAC	360		
Qy	361	CATAGTTTCTGCTAGTGGACCGT	385		
Db	361	CATAGTTTCTGCTAGTGGACCGT	385		

RESULT 6  
US-09-232-880-67  
; Sequence 67, Application US/09232880  
; Publication No. US20020182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun C.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.4280C  
; CURRENT APPLICATION NUMBER: US/09/232.880

; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-232-880-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACCTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
DB 1 ACTACACACCTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
QY 61 GGTGGGACCCAGCATTCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGGACCCAGCATTCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120  
QY 121 CCTTTTAAAAAAGGGGACTTCTTAAAAAAGAAAGTCTAGCCAGATTTGTGTAGAGCAGC 180  
DB 121 CCTTTTAAAAAAGGGGACTTCTTAAAAAAGAAAGTCTAGCCAGATTTGTGTAGAGCAGC 180  
QY 181 TGTGCTGTGCTGGAGATTCATCTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCATCTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGCACTTTGCAATGAGATGGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
DB 241 CTGGGCACTTTGCAATGAGATGGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 7

US-09-895-793-67  
; Sequence 67, Application US/09895793  
; Publication No. US20020192763A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C2  
; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-895-793-67

Query Match 100.0%; Score 385; DB 3; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTACACACCTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
DB 1 ACTACACACCTCCACTTGGCCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60  
QY 61 GGTGGGACCCAGCATTCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGGACCCAGCATTCTCATGTGCAAGATTGGCCAGCAGACATCAGGTCTGAGAGTTC 120  
QY 121 CCTTTTAAAAAAGGGGACTTCTTAAAAAAGAAAGTCTAGCCAGATTTGTGTAGAGCAGC 180  
DB 121 CCTTTTAAAAAAGGGGACTTCTTAAAAAAGAAAGTCTAGCCAGATTTGTGTAGAGCAGC 180  
QY 181 TGTGCTGTGCTGGAGATTCATCTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCATCTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
QY 241 CTGGGCACTTTGCAATGAGATGGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
DB 241 CTGGGCACTTTGCAATGAGATGGGGCTGGTCTGATCTCAGCACTCTCTTAGTCTGCTTG 300  
QY 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360  
DB 301 CCTCTCCAGGCCCCAGCCTGGCCACACCTCTTACAGGGCACTCTCAGATGCCCATAC 360  
QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 8

US-09-895-814-67  
; Sequence 67, Application US/09895814  
; Publication No. US20020193296A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C26  
; CURRENT APPLICATION NUMBER: US/09/895,814

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; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-67

Query Match      100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
    |||
Db 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
    |||

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
    |||
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
    |||

QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
    |||
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
    |||

QY 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
    |||
Db 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
    |||

QY 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTGTGATCTCAGCACTCCTTAGTCTGCTTG 300
    |||
Db 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTGTGATCTCAGCACTCCTTAGTCTGCTTG 300
    |||

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
    |||
Db 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
    |||

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
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RESULT 9
US-10-012-896-67
; Sequence 67, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
```

```
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-67

Query Match      100.0%; Score 385; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
    |||
Db 1 ACTACACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATGCTGA 60
    |||

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
    |||
Db 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGAGACATCAGGTCTGAGAGTTC 120
    |||

QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
    |||
Db 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
    |||

QY 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
    |||
Db 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240
    |||

QY 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTGTGATCTCAGCACTCCTTAGTCTGCTTG 300
    |||
Db 241 CTGGGAGCTTTGCACATGAGATGGGGCTGGTGTGATCTCAGCACTCCTTAGTCTGCTTG 300
    |||

QY 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
    |||
Db 301 CCTCTCCAGGGCCCCAGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
    |||

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385
```

```
RESULT 10
US-10-010-940-67
; Sequence 67, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-010-940-67
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Query Match 100.0%; Score 385; DB 6; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180  
DB 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
DB 241 CTGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 11

US-10-144-678A-67

; Sequence 67, Application US/10144678A

; Publication No. US20030157089A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yudi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A. W.

; APPLICANT: Hepler, William T.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals y de Bassols, Carlota

; APPLICANT: Foy, Teresa M.

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Deng, Ta

; APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C28

; CURRENT APPLICATION NUMBER: US/10/144,678A

; CURRENT FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 1033

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-144-678A-67

Query Match 100.0%; Score 385; DB 7; Length 385;

Best Local Similarity 100.0%; Pred. No. 2.2e-126;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180  
DB 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240  
DB 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240

QY 241 CTGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
DB 241 CTGGCAGTCTTGACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300

QY 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360  
DB 301 CCTCTCCAGGGCCCCAGCCTGGCCACACCTGCTTTACAGGGCACTCTCAGATGCCATAC 360

QY 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
DB 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 12

US-10-294-025-67

; Sequence 67, Application US/10294025

; Publication No. US20030185830A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Stolk, John A.

; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C29

; CURRENT APPLICATION NUMBER: US/10/294,025

; CURRENT FILING DATE: 2002-11-12

; NUMBER OF SEQ ID NOS: 1038

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67

; LENGTH: 385

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-294-025-67

Query Match 100.0%; Score 385; DB 7; Length 385;

Best Local Similarity 100.0%; Pred. No. 2.2e-126;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60  
DB 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACATTTAGGAATGCTGA 60

QY 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
DB 61 GGTGGACAGCCACATCTCATGTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120

QY 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180  
DB 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCAGATTTGTAGAGCAGC 180

QY 181 TGTGCTGTGCTGGAGATTCACTTTTGGAGAGTTCCTCTGAGACCTGATCTTTAGAGG 240



Db 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
Qy 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTCTTG 300  
Db 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTCTTG 300  
Qy 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
Db 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 13  
US-10-688-838-67  
; Sequence 67, Application US/10688838  
; Publication No. US20040141989A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; FILE REFERENCE: 210121.427D4  
; CURRENT APPLICATION NUMBER: US/10/688,838  
; CURRENT FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-688-838-67

Query Match 100.0%; Score 385; DB 8; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60  
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60  
Qy 61 GGTGGACAGCCACATCTCTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
Db 61 GGTGGACAGCCACATCTCTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
Qy 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGACAGC 180  
Db 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGACAGC 180  
Qy 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
Db 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
Qy 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTCTTG 300  
Db 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTCTTG 300  
Qy 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
Db 301 CCTCTCCAGGGCCCCAGGCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360  
Qy 361 CATAGTTTCTGTCTAGTGGACCGT 385  
Db 361 CATAGTTTCTGTCTAGTGGACCGT 385

RESULT 14  
US-11-234-786-67  
; Sequence 67, Application US/11234786  
; Publication No. US20060024301A1

GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.  
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION  
; FILE REFERENCE: 210121.427C31  
; CURRENT APPLICATION NUMBER: US/11/234,786  
; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US 09/568,857  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 09/536,857  
; PRIOR FILING DATE: 2000-05-27  
; PRIOR APPLICATION NUMBER: US 09/483,672  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: US 09/439,313  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/352,616  
; PRIOR FILING DATE: 1999-07-13  
; PRIOR APPLICATION NUMBER: US 09/288,946  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 09/232,149  
; PRIOR FILING DATE: 1999-01-15  
; PRIOR APPLICATION NUMBER: US 09/159,812  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: US 09/115,453  
; PRIOR FILING DATE: 1998-07-14  
; PRIOR APPLICATION NUMBER: US 09/030,607  
; PRIOR FILING DATE: 1998-02-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 701  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-234-786-67

Query Match 100.0%; Score 385; DB 16; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.2e-126;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60  
Db 1 ACTACACACTCCACTTGCCTTGTGAGACACTTTGTCCAGCACTTTAGGAATCTGA 60  
Qy 61 GGTGGACAGCCACATCTCTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
Db 61 GGTGGACAGCCACATCTCTGCAAGATTGCCAGCAGACATCAGGTCTGAGAGTTC 120  
Qy 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGACAGC 180  
Db 121 CCTTTTAAAAAGGGAGCTTGTCTTAAAAAGAGTCTAGCCAGGATTGTGAGACAGC 180  
Qy 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
Db 181 TGTGCTGTGCTGAGATTCACTTTTGAGAGAGTTCTCTCTGAGACCTGATCTTTAGAGG 240  
Qy 241 CTGGGAGCTTTCACATGAGATGGGCTGGTCTGATCTCAGACCTCCTTAGTCTCTTG 300

Db 241 CTGGCAGCTTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
Qy CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360  
|||||  
Db 301 CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360  
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
|||||  
Db 361 CATAGTTTCTGTGCTAGTGGACCGT 385

## RESULT 15

US-10-294-025-1036  
; Sequence 1036, Application US/10294025  
; Publication No. US20030185830A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolk, John A.  
; APPLICANT: Kalos, Michael D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C29  
; CURRENT APPLICATION NUMBER: US/10/294,025  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 1036  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1036  
; LENGTH: 3710  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-294-025-1036

Query Match 99.2%; Score 381.8; DB 7; Length 3710;  
Best Local Similarity 99.5%; Pred. No. 8.4e-125;  
Matches 383; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 60  
|||  
Db 2282 ACCACACACTCCACTTGCCCTTGTGAGACACTTTGTGCCAGCACTTTAGGAATGCTGA 2341  
Qy 61 GGTCCGACAGCCACATCTCATGTCCAGATTGCCAGCAGACATCAGTCTGAGAGTTC 120  
|||  
Db 2342 GGTCCGACAGCCACATCTCATGTCCAGATTGCCAGCAGACATCAGTCTGAGAGTTC 2401  
Qy 121 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180  
|||  
Db 2402 CCCTTTTAAAAAGGGGACTTGCCTTAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 2461  
Qy 181 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTCAGACCTGATCTTTAGAGG 240  
|||  
Db 2462 TGTGCTGTGCTGGAGATTACATTTTGGAGAGTTCCTCTCAGACCTGATCTTTAGAGG 2521  
Qy 241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300  
|||  
Db 2522 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 2581  
Qy 301 CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 360  
|||  
Db 2582 CCTCTCCAGGCCCCAGCCTGGCCACACACCTGCTTTACAGGGCACTCTCAGATGCCCATAC 2641  
Qy 361 CATAGTTTCTGTGCTAGTGGACCGT 385  
|||||  
Db 2642 CATAGTTTCTGTGCTAGTGGACCGT 2666

Search completed: December 31, 2006, 13:56:03  
Job time : 615.045 secs

GenCore version 5.1.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:26:03 ; Search time 557.33 Seconds  
(without alignments)  
6266.684 Million cell updates/sec

Title: US-09-232-880-107

Perfect score: 1621

Sequence: 1 cgcctggcactgcaggcga.....aaaaaaaaaaaaaaaaaaaa 1621

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3050214 seqs, 1077301958 residues

Total number of hits satisfying chosen parameters: 6100428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US12\_NEW\_PUB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US13\_NEW\_PUB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US14\_NEW\_PUB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US15\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1621	100.0	1621	7	US-11-344-932-107
2	1621	100.0	1621	10	US-11-349-541-107
3	1574.2	97.1	2005	8	US-11-266-748A-23190
4	1574.2	97.1	2005	10	US-11-343-797-104
5	1571	96.9	2041	8	US-11-266-748A-22797
6	1524.8	94.1	2068	8	US-11-266-748A-23899
7	1240.6	76.5	2373	8	US-11-266-748A-57286
8	882.2	54.4	971	8	US-11-266-748A-215905
9	882.2	54.4	971	8	US-11-266-748A-237887
10	783	48.3	958	8	US-11-266-748A-46436
11	734.6	45.3	924	8	US-11-266-748A-84584
12	734.6	45.3	924	8	US-11-266-748A-111891
13	734.6	45.3	924	8	US-11-266-748A-137395
14	515	31.8	537	7	US-11-344-932-74
15	515	31.8	537	10	US-11-349-541-74
16	514	31.7	554	8	US-11-266-748A-349470
17	514	31.7	554	8	US-11-266-748A-432849
18	513.6	31.7	932	8	US-11-266-748A-371009
19	513.6	31.7	932	8	US-11-266-748A-454388
20	447.8	27.6	625	10	US-11-190-172-4076
21	426.8	26.3	430	8	US-11-301-554-1504
22	424	26.2	597	7	US-11-371-354-4921

23	424	26.2	597	7	US-11-371-354-59156	Sequence 59156, A
C 24	406.6	25.1	773	7	US-11-344-932-3	Sequence 3, Appli
C 25	406.6	25.1	773	10	US-11-349-541-3	Sequence 3, Appli
26	403.2	24.9	793	7	US-11-344-932-33	Sequence 33, Appl
27	403.2	24.9	793	10	US-11-349-541-33	Sequence 33, Appl
28	400.2	24.7	816	7	US-11-344-932-2	Sequence 2, Appli
29	400.2	24.7	816	10	US-11-349-541-2	Sequence 2, Appli
C 30	275.4	17.0	301	7	US-11-344-932-252	Sequence 252, App
C 31	272.4	16.8	301	7	US-11-344-932-242	Sequence 242, App
C 32	234.8	14.5	5895	6	US-10-527-552-6	Sequence 6, Appli
33	189.4	11.7	582	8	US-11-266-748A-380888	Sequence 380888,
C 34	189.4	11.7	582	8	US-11-266-748A-464267	Sequence 464267,
C 35	121.4	7.5	1000	8	US-11-266-748A-224722	Sequence 224722,
C 36	121.4	7.5	1000	8	US-11-266-748A-246615	Sequence 246615,
C 37	121.4	7.5	1000	8	US-11-266-748A-398998	Sequence 398998,
C 38	121.4	7.5	1000	8	US-11-266-748A-470044	Sequence 470044,
C 39	104	6.4	676	8	US-11-266-748A-84585	Sequence 84585, A
40	104	6.4	676	8	US-11-266-748A-111892	Sequence 111892,
C 41	104	6.4	676	8	US-11-266-748A-137396	Sequence 137396,
C 42	81	5.0	469	10	US-11-292-078-16830	Sequence 16830, A
C 43	79.4	4.9	560	10	US-11-292-078-2253	Sequence 2253, Ap
C 44	76.8	4.7	499	10	US-11-292-078-10189	Sequence 10189, A
C 45	75.6	4.7	565	10	US-11-292-078-11125	Sequence 11125, A

#### ALIGNMENTS

#### RESULT 1

US-11-344-932-107  
; Sequence 107, Application US/11344932  
; Publication No. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Deng, Ta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C32  
; CURRENT APPLICATION NUMBER: US/11/344,932  
; CURRENT FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: 10/144,678  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 10/012,896  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 09/895,814  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/852,911  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: 09/780,669  
; PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-107

Query Match      100.0%; Score 1621; DB 7; Length 1621;
Best Local Similarity 100.0%; Pred. No. 4e-304;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGSCATGCGAGGACATCGGTTCATGGAGCTGTCGGCCCTGGCCCGGCGCGTT 60
Db |||||||
Qy 1 CGCCATGSCATGCGAGGACATCGGTTCATGGAGCTGTCGGCCCTGGCCCGGCGCGTT 60
Db |||||||

61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGCTGTGTGACGCTGGACCGGCCGCGTC 120
Db |||||||

61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGCTGTGTGACGCTGGACCGGCCGCGTC 120
Db |||||||

121 CCGCTACGAGCTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA 180
Db |||||||

121 CCGCTACGAGCTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA 180
Db |||||||

181 GCCGGGGAGCGCGCTGCGGCGCTGTGCAAGCGGTCGGATGCTGCTGGAGCC 240
Db |||||||

181 GCCGGGGAGCGCGCTGCGGCGCTGTGCAAGCGGTCGGATGCTGCTGGAGCC 240
Db |||||||

241 CTTCCGCGCGGCTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCCTGACGCGGAAA 300
Db |||||||

241 CTTCCGCGCGGCTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCCTGACGCGGAAA 300
Db |||||||

301 TCCAAAGGCTTATTTAGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT 360
Db |||||||

301 TCCAAAGGCTTATTTAGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT 360
Db |||||||

361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAG 420
Db |||||||

361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAG 420
Db |||||||

421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCTCGGCTGACTTTGCTGGTGGCTTTAT 480
Db |||||||

421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCTCGGCTGACTTTGCTGGTGGCTTTAT 480
Db |||||||

481 GTGTGCACTGGGCATTTAATGGCTCTTTTGAACCGCAACGCACTGAAGGTCAGGT 540
Db |||||||

481 GTGTGCACTGGGCATTTAATGGCTCTTTTGAACCGCAACGCACTGAAGGTCAGGT 540
Db |||||||

541 CATTGATCCAAATATGGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600
Db |||||||

541 CATTGATCCAAATATGGTGGAGGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600
Db |||||||

601 GAAATCGAGTCTGTGGGAGCACCCTCGAGGACAGAACTGTTGGATGGTGAGCACCCTT 660
Db |||||||

601 GAAATCGAGTCTGTGGGAGCACCCTCGAGGACAGAACTGTTGGATGGTGAGCACCCTT 660
Db |||||||

661 CTATACGACTTACAGGACAGCAATGGGAATTCATGGCTGTGTGGCAATAGAACCCCA 720
Db |||||||

661 CTATACGACTTACAGGACAGCAATGGGAATTCATGGCTGTGTGGCAATAGAACCCCA 720
Db |||||||

721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAGTCTGATGAATTCCTCAATCAGAT 780
Db |||||||
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RESULT 2  
US-11-349-541-107  
; Sequence 107, Application US/11349541  
; Publication No. US20060223129A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND  
; TITLE OF INVENTION: METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.428C7

Db 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT 780  
Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAGATTTGAGATGATTTGCGAAGAGAC 840  
Db |||||||  
Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAGATTTGAGATGATTTGCGAAGAGAC 840  
Qy 841 GAAGGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCAGAC 900  
Db |||||||  
Db 841 GAAGGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCAGAC 900  
Qy 901 TTTTGGAGAGTGTTCATCATGATCAACAAGGAAACGGGCTCGTTTATCAACAGTGA 960  
Db |||||||  
Db 901 TTTTGGAGAGTGTTCATCATGATCAACAAGGAAACGGGCTCGTTTATCAACAGTGA 960  
Qy 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTTTAAACACCCCGACCTCCCTTC 1020  
Db |||||||  
Db 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTTTAAACACCCCGACCTCCCTTC 1020  
Qy 1021 TTTCAAAAGGGATCTCTTTCATAGGAGAACACACTGAGGAGATCTTCAAGAAATTTGGATT 1080  
Db |||||||  
Db 1021 TTTCAAAAGGGATCTCTTTCATAGGAGAACACACTGAGGAGATCTTCAAGAAATTTGGATT 1080  
Qy 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140  
Db |||||||  
Db 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140  
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCCAACGGCTCAAGTGAATTTGAATCTGATTTACAGTG 1200  
Db |||||||  
Db 1141 AGCTAGTCTCTAACTTCCAGGCCCAACGGCTCAAGTGAATTTGAATCTGATTTACAGTG 1200  
Qy 1201 TAGAGTAAACATATAAATCTGATGCAATGGAACATGAGGAAACAGATTTACAGTGTCTTA 1260  
Db |||||||  
Db 1201 TAGAGTAAACATATAAATCTGATGCAATGGAACATGAGGAAACAGATTTACAGTGTCTTA 1260  
Qy 1261 CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAATTTCTAAA 1320  
Db |||||||  
Db 1261 CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAATTTCTAAA 1320  
Qy 1321 AATGGTTATCAATAGGCTTTTGAATTTATAAACTTTGGGTACTTATCTAAATATAGGT 1380  
Db |||||||  
Db 1321 AATGGTTATCAATAGGCTTTTGAATTTATAAACTTTGGGTACTTATCTAAATATAGGT 1380  
Qy 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440  
Db |||||||  
Db 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440  
Qy 1441 TTTTGAATGGGTTCTAGTGAAAGGAATGATATTTCTTTGAAGACATCGATATACATTT 1500  
Db |||||||  
Db 1441 TTTTGAATGGGTTCTAGTGAAAGGAATGATATTTCTTTGAAGACATCGATATACATTT 1500  
Qy 1501 ATTTTACATCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCCAAAATTTGATGGTGAT 1560  
Db |||||||  
Db 1501 ATTTTACATCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCCAAAATTTGATGGTGAT 1560  
Qy 1561 ARAAGTCAAGTGAACCAAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAA 1620  
Db |||||||  
Db 1561 ARAAGTCAAGTGAACCAAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAA 1620  
Qy 1621 A 1621  
Db 1621 A 1621

CURRENT APPLICATION NUMBER: US/11/349,541  
CURRENT FILING DATE: 2006-02-06  
PRIOR APPLICATION NUMBER: US 09/116,134  
PRIOR FILING DATE: 1998-07-14  
PRIOR APPLICATION NUMBER: US 09/030,606  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: US 09/020,747  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 08/904,809  
PRIOR FILING DATE: 1997-08-01  
PRIOR APPLICATION NUMBER: US 08/806,596  
PRIOR FILING DATE: 1997-02-25  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 107  
LENGTH: 1621  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-349-541-107

Query Match 100.0%; Score 1621; DB 10; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 4e-304;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGCAGGCACTTCGGTCTATGGAGCTGTCCGGCTGGCCCGCGGCCGCTT 60  
DB 1 CGCCATGGCACTGCAGGCACTTCGGTCTATGGAGCTGTCCGGCTGGCCCGCGGCCGCTT 60

QY 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGGTACGCTGGGACCGGCGCGGCTC 120  
DB 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGGTACGCTGGGACCGGCGCGGCTC 120

QY 121 CGCTACGACGTGAGCGCTTCGGCGCGGCGGTGTGGTACGCTGGGACCGGCGCGGCTC 180  
DB 121 CGCTACGACGTGAGCGCTTCGGCGCGGCGGTGTGGTACGCTGGGACCGGCGCGGCTC 180

QY 181 GCGCGGGGAGCGCGCTGCTGCGGCTGTGTCAGAGCGGTGGATGCTGCTGGAGCC 240  
DB 181 GCGCGGGGAGCGCGCTGCTGCGGCTGTGTCAGAGCGGTGGATGCTGCTGGAGCC 240

QY 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCGCCAGAGATTCTCAGCGGGA 300  
DB 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCGCCAGAGATTCTCAGCGGGA 300

QY 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTGGCCAGTCCAGAGCTTCTGCGGTT 360  
DB 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTGGCCAGTCCAGAGCTTCTGCGGTT 360

QY 361 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAG 420  
DB 361 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAG 420

QY 421 TGGTGAGAAATCCGTATGCCCCCTGAATCTCCTGGCTGACTTTGCTGGTGGGCTTAT 480  
DB 421 TGGTGAGAAATCCGTATGCCCCCTGAATCTCCTGGCTGACTTTGCTGGTGGGCTTAT 480

QY 481 GTGTGACCTGGGCAATTAATGGCTCTTTTGGACCGCACACGCTGCAAGGGTCAGT 540  
DB 481 GTGTGACCTGGGCAATTAATGGCTCTTTTGGACCGCACACGCTGCAAGGGTCAGT 540

QY 541 CATTTGATGCAAAATATGGTGGAGGACACGATATTTAAGTCTTTTCTGGGAAACTCA 600  
DB 541 CATTTGATGCAAAATATGGTGGAGGACACGATATTTAAGTCTTTTCTGGGAAACTCA 600

QY 601 GAAATCGAGTCTGTGGGAGGACCTTCAGGACAGAACTGTTGGATGGTGGAGCACCTTT 660  
DB 601 GAAATCGAGTCTGTGGGAGGACCTTCAGGACAGAACTGTTGGATGGTGGAGCACCTTT 660

QY 661 CTATAGCACTTACAGACAGCAGATGGGAAATTCATGGCTGTGTGGGCAATAGACCCCA 720  
DB 661 CTATAGCACTTACAGACAGCAGATGGGAAATTCATGGCTGTGTGGGCAATAGACCCCA 720

QY 721 GTTCTACGAGCTGCTGATCAAGGACCTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 780

DB 721 GTTCTACGAGCTGCTGATCAAGGACCTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 780

QY 781 GAGCATGATGATTCGCCAGAAATCAAGAAGTTTCAGATGATTTTTCAGAAAGAC 840

DB 781 GAGCATGATGATTCGCCAGAAATCAAGAAGTTTCAGATGATTTTTCAGAAAGAC 840

QY 841 GAAAGCAGATGCTGTCAAACTTTTGACGGCAGACAGATGCTGTGACTCCGGTCTGAC 900

DB 841 GAAAGCAGATGCTGTCAAACTTTTGACGGCAGACAGATGCTGTGACTCCGGTCTGAC 900

QY 901 TTTTCAGAGGTTGTTTCATCATGATCAAAAGGAAACGGGCTGTTTATCAGCATGA 960

DB 901 TTTTCAGAGGTTGTTTCATCATGATCAAAAGGAAACGGGCTGTTTATCAGCATGA 960

QY 961 GGAGCAGACGTGAGCGCCCGCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC 1020

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DB 1021 TTTCAAAAGGGATCCCTTTTCATAGGAGAACACACTGAGGAGATATCTTGAAGATTTGGATT 1080

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DB 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAAGTAAGTAAA 1140

QY 1141 AGCTAGTCTTAACTTCCAGGCGCCAGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200

DB 1141 AGCTAGTCTTAACTTCCAGGCGCCAGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200

QY 1201 TAGAGTAAACATAAATCTTGTATGATGGAACATGGAGAACAGTATTACAGTGTCTTA 1260

DB 1201 TAGAGTAAACATAAATCTTGTATGATGGAACATGGAGAACAGTATTACAGTGTCTTA 1260

QY 1261 CCACCTCTAATCAAGAAAGAAATTAAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1320

DB 1261 CCACCTCTAATCAAGAAAGAAATTAAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1320

QY 1321 AATGGTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATTTGTT 1380

DB 1321 AATGGTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATTTGTT 1380

QY 1381 AGTTATCTGCTTCCAGTCTTGTATATTTTGTGATATTAAGATTTCTTGAATTTATATA 1440

DB 1381 AGTTATCTGCTTCCAGTCTTGTATATTTTGTGATATTAAGATTTCTTGAATTTATATA 1440

QY 1441 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500

DB 1441 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500

QY 1501 ATTTACACTCTTGAATTTACAAATGAGAAATGAGAAATGCCAATAATTTGATGGTAT 1560

DB 1501 ATTTACACTCTTGAATTTACAAATGAGAAATGAGAAATGCCAATAATTTGATGGTAT 1560

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DB 1561 AAAAGTCACTGACAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620

QY 1621 A 1621

DB 1621 A 1621

## RESULT 3

US-11-266-748A-23190  
; Sequence 23190, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and

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; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55015-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23190
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-23190

Query Match          97.1%; Score 1574.2; DB 8; Length 2005;
Best Local Similarity 99.8%; Pred No. 4, 7e-295;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1  CGCCATGGCACTGCAGGGCACTCTGGTCAATGAGCTGTCCGGCTTGGCCCGGGCCCGGTT 60
Db 62  CGCCATGGCACTGCAGGGCACTCTGGTCTGTGGAGCTGTCCGGCTTGGCCCGGGCCCGGTT 121
Qy 61  CTGTGCTATGGTCTGTGGTGTGCTTGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 122  CTGTGCTATGGTCTGTGGTGTGCTTCTGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 181
Qy 121  CGGCTACCACTGAGCCGCTTGGGCGGGGCAAGGCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 182  CGGCTACCACTGAGCCGCTTGGGCGGGGCAAGGCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241
Qy 181  GCCCGGGGAGCCCGGCTGTGCGCGTCTGTGCAAGCGGTCTGGATGTGTGTGTGTGTGTGTGTGT 240
Db 242  GCCCGGGGAGCCCGGCTGTGCGCGTCTGTGCAAGCGGTCTGGATGTGTGTGTGTGTGTGTGTGT 301
Qy 241  CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCGCCAGAGATTCTGACGCGGGAATA 300
Db 302  CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCGCCAGAGATTCTGACGCGGGAATA 361
Qy 301  TCCAAAGGCTTATTTATGCCAGCTCAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTT 360
Db 362  TCCAAAGGCTTATTTATGCCAGCTCAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTT 421
Qy 361  AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAG 420
Db 422  AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAG 481
Qy 421  TGGTGAGAACTCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGTGGCTTAT 480
Db 482  TGGTGAGAACTCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGTGGCTTAT 541
Qy 481  GTGTGCACTGGGCATTATAAATGGCTCTTTTGAACGCAACGCACTGCAAGGGTCAGGT 540
Db 542  GTGTGCACTGGGCATTATAAATGGCTCTTTTGAACGCAACGCACTGCAAGGGTCAGGT 601
Qy 541  CATTCATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTCTTTTCTGTGGAATACTCA 600
Db 602  CATTCATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTCTTTTCTGTGGAATACTCA 661
Qy 601  GAAATCGAGTCTGTGGGAGACCTTCGAGGACAGAACTGTGGATGTGGAGCACCTTT 660

662  GAAATCGAGTCTGTGGGAGACCTTCGAGGACAGAACTGTGGATGTGGAGCACCTTT 721
Qy 661  CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAAACCCCA 720
Db 722  CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAAACCCCA 781
Qy 721  GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGTAGTAACTCCCAATCAGAT 780
Db 782  GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGTAGTAACTCCCAATCAGAT 841
Qy 781  GAGCATGATGATTGGCCAGAAATGAAGAAAGATTGTCAGATGATTTTGCAAAAGAAAGAC 840
Db 842  GAGCATGATGATTGGCCAGAAATGAAGAAAGATTGTCAGATGATTTTGCAAAAGAAAGAC 901
Qy 841  GAAAGGACAGTGTGTCAAAATCTTTTGACGACAGATGCTGTGTGTGTGTGTGTGTGTGTGTGAC 900
Db 902  GAAAGGACAGTGTGTCAAAATCTTTTGACGACAGATGCTGTGTGTGTGTGTGTGTGTGTGTGAC 961
Qy 901  TTTTGAGGAGTGTTCATCATGATCAACACAGGACGGGCTCGTTTATCACCAGTGA 960
Db 962  TTTTGAGGAGTGTTCATCATGATCAACACAGGACGGGCTCGTTTATCACCAGTGA 1021
Qy 961  GGAGCAGAGCTGAGCCCGCCCTGCACTCTGCTGTAAACACACCCAGCCATCCCTTC 1020
Db 1022  GGAGCAGAGCTGAGCCCGCCCTGCACTCTGCTGTAAACACACCCAGCCATCCCTTC 1081
Qy 1021  TTTCAAAAGGATCTTTTCATAGAGAAACAACATGAGAGATCTTGAAGAAATTTGATTT 1080
Db 1082  TTTCAAAAGGATCTTTTCATAGAGAAACAACATGAGAGATCTTGAAGAAATTTGATTT 1141
Qy 1081  CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140
Db 1142  CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1201
Qy 1141  AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1200
Db 1202  AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1261
Qy 1201  TAGAGTAACACATAAATTTGTATGATGGAACATGAGGAAACAGTATTAACAGTGTCTTA 1260
Db 1262  TAGAGTAACACATAAATTTGTATGATGGAACATGAGGAAACAGTATTAACAGTGTCTTA 1321
Qy 1261  CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAAATTTCTAAA 1320
Db 1322  CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAAATTTCTAAA 1381
Qy 1321  AATGGTTATCAATTAAGGCTTTTGTATTTATAAAAATTTGGGTACTTATACTAAATATAGGT 1380
Db 1382  AATGGTTATCAATTAAGGCTTTTGTATTTATAAAAATTTGGGTACTTATACTAAATATAGGT 1441
Qy 1381  AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTGATATTAAGATTTCTTGATATATA 1440
Db 1442  AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTGATATTAAGATTTCTTGATATATA 1501
Qy 1441  TTTTGAATGGTCTTAGTGAAGAAAGATGATATTTCTTGAACACATCGATATACATTT 1500
Db 1502  TTTTGAATGGTCTTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1561
Qy 1501  ATTTTACACTCTTGAATCTTACAAATGAGAAATGAGAAATGCCCAAAATTTGTATGGTGAT 1560
Db 1562  ATTTTACACTCTTGAATCTTACAAATGAGAAATGAGAAATGCCCAAAATTTGTATGGTGAT 1621
Qy 1561  AAAAGTCACGTGAAACAAA 1579
Db 1622  AAAAGTCACGTGAAACAGA 1640

RESULT 4
US-11-343-797-104
; Sequence 104, Application US/11343797
; Publication No. US20060211017A1
; GENERAL INFORMATION:
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APPLICANT: Chinmalyan, Arul M.  
APPLICANT: Rubin, Mark A.  
APPLICANT: Sreekumar, Arun  
TITLE OF INVENTION: Expression Profile of Prostate Cancer  
FILE REFERENCE: UM-07221  
CURRENT APPLICATION NUMBER: US/11/343,797  
CURRENT FILING DATE: 2006-01-31  
PRIORITY APPLICATION NUMBER: US/10/210,120  
PRIORITY FILING DATE: 2002-08-01  
PRIORITY APPLICATION NUMBER: US 60/309,581  
PRIORITY FILING DATE: 2001-08-02  
PRIORITY APPLICATION NUMBER: US 60/334,468  
PRIORITY FILING DATE: 2001-11-15  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 104  
LENGTH: 2005  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-343-797-104

Query Match 97.1%; Score 1574.2; DB 10; Length 2005;  
Best Local Similarity 99.8%; Pred. No. 4,7e-295;  
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGCAGGCAATCTCGGTTCATGGAGCTGTCCGGCTTCGGCCCGGGCCCGGTT 60  
DB 62 CGCCATGGCACTGCAGGCAATCTCGGTTCATGGAGCTGTCCGGCTTCGGCCCGGGCCCGGTT 121

QY 61 CTGTGCTATGGTCTCGGTGACTTCGGGGCGGTGTGGTACGCGTGGACCGGCCCGGCTC 120  
DB 122 CTGTGCTATGGTCTCGGTGACTTCGGGGCGGTGTGGTACGCGTGGACCGGCCCGGCTC 181

QY 121 CGCTACGAGCTGAGCGGCTTCGGCCGGGCAAGCGCTCGTAGTCTGGACTGAAGCA 180  
DB 182 CGCTACGAGCTGAGCGGCTTCGGCCGGGCAAGCGCTCGTAGTCTGGACTGAAGCA 241

QY 181 GCGCGGGGAGCGCGGTCTGCGGGCTCTGTGCAAGCGTTCGATGCTGCTGGAGCC 240  
DB 242 GCGCGGGGAGCGCGGTCTGCGGGCTCTGTGCAAGCGTTCGATGCTGCTGGAGCC 301

QY 241 CTTCCGCCCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGACGGGAAA 300  
DB 302 CTTCCGCCCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGACGGGAAA 361

QY 301 TCCAGGCTTATTTATGCCAGCTGAGTGAATTTGCCAGTCAAGAACTTCGCCGGTT 360  
DB 362 TCCAGGCTTATTTATGCCAGCTGAGTGAATTTGCCAGTCAAGAACTTCGCCGGTT 421

QY 361 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGCTTCTCAAAAATTTGGCAGAAG 420  
DB 422 AGCTGCCACGATATCAACTATTTGGCTTTGTGAGGCTTCTCAAAAATTTGGCAGAAG 481

QY 421 TGGTGAGATTCGGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTAT 480  
DB 482 TGGTGAGATTCGGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTAT 541

QY 481 GTGTGACTGGGCAATTTAATGGCTCTTTTGGACGCAACGCACTGAAGGTCAGGT 540  
DB 542 GTGTGACTGGGCAATTTAATGGCTCTTTTGGACGCAACGCACTGAAGGTCAGGT 601

QY 541 CATTTGATGCAATATGCTGGAGGAACAGCATATTTAAGTCTTTTCTGGGAACTCA 600  
DB 602 CATTTGATGCAATATGCTGGAGGAACAGCATATTTAAGTCTTTTCTGGGAACTCA 661

QY 601 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 660  
DB 662 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 721

QY 661 CTATACGATTTACGAGCAAGCATGGGAAATTCATGGCTGTGTGGAGCAATGAAGCCCA 720  
DB 722 CTATACGATTTACGAGCAAGCATGGGAAATTCATGGCTGTGTGGAGCAATGAAGCCCA 781

QY 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACATTTCCCAATCAGAT 780  
DB 782 GTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACATTTCCCAATCAGAT 841

QY 781 GAGCATGATGATTTGGCCAGAAATGAAGAAGATTTGACAGATGATATTTGCAAGAAGAC 840  
DB 842 GAGCATGATGATTTGGCCAGAAATGAAGAAGATTTGACAGATGATATTTGCAAGAAGAC 901

QY 841 GAAGCAGAGTGTGTGCTCAAACTTTTGACGCGACAGATGCTGTGTGACTCCGGTTCCTGAC 900  
DB 902 GAAGCAGAGTGTGTGCTCAAACTTTTGACGCGACAGATGCTGTGTGACTCCGGTTCCTGAC 961

QY 901 TTTTGAGGAGGTTGTTTCATCATGATCAACAAGGAACCGGCTCGTTTATCACCACTGA 960  
DB 962 TTTTGAGGAGGTTGTTTCATCATGATCAACAAGGAACCGGCTCGTTTATCACCACTGA 1021

QY 961 GGAGCAGGACGTGAGCCCGCCCGCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC 1020  
DB 1022 GGAGCAGGACGTGAGCCCGCCCGCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC 1081

QY 1021 TTTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTTGAAGAAATTTGGATT 1080  
DB 1082 TTTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTTGAAGAAATTTGGATT 1141

QY 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAA 1140  
DB 1142 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAA 1201

QY 1141 AGCTAGTCTCTAACTTCAGGCCACGGCTCAAGTGAATTTGAAATACTGATTTACAGTG 1200  
DB 1202 AGCTAGTCTCTAACTTCAGGCCACGGCTCAAGTGAATTTGAAATACTGATTTACAGTG 1261

QY 1201 TAGAGTAAACATAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
DB 1262 TAGAGTAAACATAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321

QY 1261 CCACCTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320  
DB 1322 CCACCTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1381

QY 1321 AATGGTATCATTAGGGCTTTTGAATTTAATAAACTTTGGGTACTTATACATAATTTATGGT 1380  
DB 1382 AATGGTATCATTAGGGCTTTTGAATTTAATAAACTTTGGGTACTTATACATAATTTATGGT 1441

QY 1381 AGTTATCTGCTTCCAGTTTCTGATATTTTGTGATATTAAGATTTCTGACTTATA 1440  
DB 1442 AGTTATCTGCTTCCAGTTTCTGATATTTTGTGATATTAAGATTTCTGACTTATA 1501

QY 1441 TTTTGAATGGGTTCTAGTGAAGAAAAGAAATGATATTTCTTGAAGACATCGATATACATTT 1500  
DB 1502 TTTTGAATGGGTTCTAGTGAAGAAAAGAAATGATATTTCTTGAAGACATCGATATACATTT 1561

QY 1501 ATTTACACTTTGATTTCAATGTAGAAAATGAGAAAATGCCAANAATTTGATGATGAT 1560  
DB 1562 ATTTACACTTTGATTTCAATGTAGAAAATGAGAAAATGCCAANAATTTGATGATGAT 1621

QY 1561 AAAAGTCAGTGAAGACAAA 1579  
DB 1622 AAAAGTCAGTGAAGACAAA 1640

RESULT 5  
US-11-266-748A-22797  
; Sequence 22797, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnstone, Paul  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcription Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A







;; TITLE OF INVENTION: Transcriptome Microarray Technology and  
;; FILE REFERENCE: 55815-0102 (319189)  
;; CURRENT APPLICATION NUMBER: US/11/266,748A  
;; CURRENT FILING DATE: 2005-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105479.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105482.6  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105483.4  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105507.0  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105485.9  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105484.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: US 60/662,276  
;; PRIOR FILING DATE: 2005-03-14  
;; PRIOR APPLICATION NUMBER: US 60/700,293  
;; PRIOR FILING DATE: 2005-07-18  
;; NUMBER OF SEQ ID NOS: 483996  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 23899

;; TYPE: DNA

;; ORGANISM: Homo Sapiens

;; FEATURE:

;; NAME/KEY: misc.feature

;; LOCATION: (143)..(143)

;; OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-23899

Query Match 94.1%; Score 1524.8; DB 8; Length 2068;

Best Local Similarity 98.6%; Pred. No. 1.7e-285;

Matches 1559; Conservative 0; Mismatches 18; Indels 4; Gaps 2;

Qy	539	GTCAATGATGCAAAATATGTTGGAAGAAACAGCATATTTAAGTCTCTTTCTGTGGAACCT	598
Db	623	GTCAATGATGCAAAATATGTTGGAAGAAACAGCATATTTAAGTCTCTTTCTGTGGAACCT	682
Qy	599	CAGAAATCGAGTCTGTGGAAGAACCTCGAGGACAGACATGTTGATGTTGGAGGACCT	658
Db	683	CAGAAATCGAGTCTGTGGAAGAACCTCGAGGACAGACATGTTGATGTTGGAGGACCT	742
Qy	659	TTCTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACC	718
Db	743	TTCTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACC	802
Qy	719	CAGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCTCCCAATCAG	778
Db	803	CAGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCTCCCAATCAG	862
Qy	779	ATGACATGATGATGTTGGCCAGAAATGAAGAAGATTTGCAGATGTTTGCAGAAAGAG	838
Db	863	ATGACATGATGATGTTGGCCAGAAATGAAGAAGATTTGCAGATGTTTGCAGAAAGAG	922
Qy	839	ACGAAGGACAGATGGTGTCAAATCTTTCACGSCACAGATGCTGTGACTCCGGTCTG	898
Db	923	ACGAAGGACAGATGGTGTCAAATCTTTCACGSCACAGATGCTGTGACTCCGGTCTG	982
Qy	899	ACTTTTGAGGAGTGTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGT	958
Db	983	ACTTTTGAGGAGTGTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGT	1042
Qy	959	GAGGACAGGACGTGAGCCCGCCCTGCACTCTGCTGTTTAAACACCCAGCCATCCCT	1018
Db	1043	GAGGACAGGACGTGAGCCCGCCCTGCACTCTGCTGTTTAAACACCCAGCCATCCCT	1102
Qy	1019	TCCTTTCAAAGGGATCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTGGA	1078
Db	1103	TCCTTTCAAAGGGATCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTGGA	1162
Qy	1079	TTCAAGCCGAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAATAGGTA	1138
Db	1163	TTCAAGCCGAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAATAGGTA	1222
Qy	1139	AAAGCTAGTCTTAATCTCCAGGCCCAAGGCTCAAGTGAATTTGAATTAATGATTTACAG	1198
Db	1223	AAAGCTAGTCTTAATCTCCAGGCCCAAGGCTCAAGTGAATTTGAATTAATGATTTACAG	1282
Qy	1199	TGTAGATTAACACATTAACATTTGATGATGAGAACATCGAGGAAACAGTATTACAGTCC	1258
Db	1283	TGTAGATTAACACATTAACATTTGATGATGAGAACATCGAGGAAACAGTATTACAGTCC	1342
Qy	1259	TACCACTCTAATCAAGAAAGAAATTAACAGATCTGATTTACAGTGAATTTGAATTTCTA	1318
Db	1343	TACCACTCTAATCAAGAAAGAAATTAACAGATCTGATTTACAGTGAATTTGAATTTCTA	1402
Qy	1319	AAATGTTTATCATTTAGGCTTTTGAATTTAATAAATCTTTGGGTACTTATACATAATATG	1378
Db	1403	AAATGTTTATCATTTAGGCTTTTGAATTTAATAAATCTTTGGGTACTTATACATAATATG	1462
Qy	1379	GTAGTTATTCGCTTCCAGTTTGCATATATTTGTTGATATTTAAGATTTCTGACTTA	1438
Db	1463	GTAGTTATTCGCTTCCAGTTTGCATATATTTGTTGATATTTAAGATTTCTGACTTA	1522
Qy	1439	TATTTGAATGGTTCAGTGAAGAAAGTATATTTCTTGAAGACATCGATATACAT	1498
Db	1523	TATTTGAATGGTTCAGTGAAGAAAGTATATTTCTTGAAGACATCGATATACAT	1582
Qy	1499	TTATTTACACTCTTGAATTTCAATGTAGAAATGAGGAAATGCCAAATTTGATGGTG	1558
Db	1583	TTATTTACACTCTTGAATTTCAATGTAGAAATGAGGAAATGCCAAATTTGATGGTG	1642
Qy	1559	ATAAAGTCAGTGAACAAA	1579
Db	1643	ATAAAGTCAGTGAACAAA	1663

## RESULT 7

US-11-266-748A-57286  
; Sequence 57286, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 57286  
; LENGTH: 2373  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-57286

Query Match 76.5%; Score 1240.6; DB 8; Length 2373;  
Best Local Similarity 89.6%; Pred. No. 1.6e-230;  
Matches 1414; Conservative 0; Mismatches 4; Indels 161; Gaps 1;  
Qy 1 CGCATGCGCATCTGAGGCGCATCTCGTCTATGAGTCTGCGGCTGCGCCCGGCGCCGTT 60  
Db |||||  
Qy 79 CGCATGCGCATCTGAGGCGCATCTCGTCTGAGTCTGCGGCTGCGCCCGGCGCCGTT 138  
Db |||||  
Qy 61 CTGTCTATGTCCTGCTGATCTTGGGGCGCGTGTGTACGCGTGGACCGGCGCGCTC 120  
Db |||||  
Qy 139 CTGTCTATGTCCTGCTGATCTTGGGGCGCGTGTGTACGCGTGGACCGGCGCGCTC 198  
Db |||||  
Qy 121 CGGTACGACGTGAGCGCTTGGGCGGCGGCAAGCGCTCGTGTGAGCTTGAAGCA 180  
Db |||||  
Qy 199 CCGTACGACGTGAGCGCTTGGGCGGCGGCAAGCGCTCGTGTGAGCTTGAAGCA 258  
Db |||||  
Qy 181 GCCGGGGAGCGCGCTGCTGCGCGCTGTGCAAGCGGTGCGATGCTGCTGGAGCC 240  
Db |||||  
Qy 259 GCCGGGGAGCGCGCTGCTGCGCGCTGTGCAAGCGGTGCGATGCTGCTGGAGCC 318  
Db |||||  
Qy 241 CTTCGCGCGCGTGTCTATGAGAACTCCAGTGGGCGCCAGAGATTCTGACGCGGAAA 300  
Db |||||  
Qy 319 CTTCGCGCGCGTGTCTATGAGAACTCCAGTGGGCGCCAGAGATTCTGACGCGGAAA 378  
Db |||||  
Qy 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCGCAGTCAGGAGCTTCTGCGGTT 360  
Db |||||  
Qy 379 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCGCAGTCAGGAGCTTCTGCGGTT 438  
Db |||||  
Qy 361 AGCTGGCCAGCATCAACTATTTGGCTTGTCTGAGTGTCTCTCAAAAATTGGCAGAAG 420  
Db |||||  
Qy 439 AGCTGGCCAGCATCAACTATTTGGCTTGTCTGAGTGTCTCTCAAAAATTGGCAGAAG 472  
Db |||||  
Qy 421 TGGTGAAGATCCGTATGCGCGCTGAACTCTCTGCGCTGACTTTGCTGGTGGCTTAT 480  
Db |||||  
Qy 473 ----- 472

Qy 481 GTGTGCACTGGGCATTATATGCTCTTTTGTGACCGCACACGCACTGACAAGGTCAGGT 540  
Db ----- 472  
Qy 541 CATTTGATCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTTCTTTTCTGTGGAATACTCA 600  
Db |||||  
Qy 473 -----GTTGGAAGGAAACAGCATATTTAAAGTTCTTTTCTGTGGAATACTCA 517  
Db |||||  
Qy 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAACATGTTGGAGTGTGGACACCTTT 660  
Db |||||  
Qy 518 GAAATTTGAGTCTGTGGGAAGCACTCGAGGACAGAAACATGTTGGAGTGTGGACACCTTT 577  
Db |||||  
Qy 661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA 720  
Db |||||  
Qy 578 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA 637  
Db |||||  
Qy 721 GTTCTACGAGCTCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT 780  
Db |||||  
Qy 638 GTTCTACGAGCTCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT 697  
Db |||||  
Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAGATTTGCGAGATGTTTTCBAAGAGAC 840  
Db |||||  
Qy 698 GAGCATGGATGATGGCCAGAAATGAAGAAGATTTGCGAGATGTTTTCBAAGAGAC 757  
Db |||||  
Qy 841 GAAGGACAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGAC 900  
Db |||||  
Qy 758 GAAGGACAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGAC 817  
Db |||||  
Qy 901 TTTTGGAGGAGTTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA 960  
Db |||||  
Qy 818 TTTTGGAGGAGTTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACCAGTGA 877  
Db |||||  
Qy 961 GGAGCAGGACGTGAGCGCCCGCTGCACTCTGTCTGTTTAAACACCCCGACCTCCCTTC 1020  
Db |||||  
Qy 878 GGAGCAGGACGTGAGCGCCCGCTGCACTCTGTCTGTTTAAACACCCCGACCTCCCTTC 937  
Db |||||  
Qy 1021 TTTTCAAAAGGATCTTTTATAGGAGAAACACTGAGGAGATATCTTCAAGAATTTGAGTT 1080  
Db |||||  
Qy 938 TTTTCAAAAGGATCTTTTATAGGAGAAACACTGAGGAGATATCTTCAAGAATTTGAGTT 997  
Db |||||  
Qy 1081 CAGCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140  
Db |||||  
Qy 998 CAGCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1057  
Db |||||  
Qy 1141 AGCTAGTCTCTAACTTCCAGGCGCCCGCTCAAGTGAATTTGATATCGATTTTACAGTG 1200  
Db |||||  
Qy 1058 AGCTAGTCTCTAACTTCCAGGCGCCCGCTCAAGTGAATTTGATATCGATTTTACAGTG 1117  
Db |||||  
Qy 1201 TAGAGTAAACATAAATCTGTATGCAATGGAACATGAGGAAACAGTATTACAGTGTCTTA 1260  
Db |||||  
Qy 1118 TAGAGTAAACATAAATCTGTATGCAATGGAACATGAGGAAACAGTATTACAGTGTCTTA 1177  
Db |||||  
Qy 1261 CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTACAGTGAATGAAATTTTAAA 1320  
Db |||||  
Qy 1178 CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTACAGTGAATGAAATTTTAAA 1237  
Db |||||  
Qy 1321 AATGGTTATCATTTAGGCTTTTGAATTTTAAACTTTGGGTAATTTACTTAAATATGTT 1380  
Db |||||  
Qy 1238 AATGGTTATCATTTAGGCTTTTGAATTTTAAACTTTGGGTAATTTACTTAAATATGTT 1297  
Db |||||  
Qy 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTATTAAGATTTCTTGAATTTATA 1440  
Db |||||  
Qy 1298 AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTATTAAGATTTCTTGAATTTATA 1357  
Db |||||  
Qy 1441 TTTTGAATGGGTTCTAGTGAAGAAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1500  
Db |||||  
Qy 1358 TTTTGAATGGGTTCTAGTGAAGAAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1417  
Db |||||  
Qy 1501 ATTTTACATCTGTTGATTTCTACAAATGAGGAAATGAGGAAATGCCACAAATTTGTATGGTAT 1560  
Db |||||  
Qy 1418 ATTTTACATCTGTTGATTTCTACAAATGAGGAAATGAGGAAATGCCACAAATTTGTATGGTAT 1477  
Db |||||  
Qy 1561 AAAAGTCACGTGAACAAA 1579





; NAME/KEY: misc.feature  
; LOCATION: (709)..(709)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-46436

Query Match 48.3%; Score 783; DB 8; Length 958;  
Best Local Similarity 95.8%; Pred. No. 3.7e-142;  
Matches 858; Conservative 0; Mismatches 31; Indels 7; Gaps 5;

QY 675 GGACACGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 734  
DB 12 GGACACGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 70  
QY 735 TGATCAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGACATGGATGAT 794  
DB 71 TGATCAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGACATGGATGAT 130  
QY 795 GGCCAGAAATGAAGAAAGTTTGCAGATGATTTTGCAGAAAGACGAAAGGAGATGAT 854  
DB 131 GGCCAGAAATGAAGAAAGTTTGCAGATGATTTTGCAGAAAGACGAAAGGAGATGAT 190  
QY 855 GTCAATCTTTCAGCGCACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 914  
DB 191 GTCAATCTTTCAGCGCACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 250  
QY 915 TTTCATCATGATCAACAAAGGAACGGGGCTCGTTTATCACAGTGAAGGAGGAGTGA 974  
DB 251 TTTCATCATGATCAACAAAGGAACGGGGCTCGTTTATCACAGTGAAGGAGGAGTGA 310  
QY 975 GCGCCCGCCCTGCACCTCTGCTGTGTTAAACACCCCGCCATCCCTCTTTCAAAGGGATC 1034  
DB 311 GCGCCCGCCCTGCACCTCTGCTGTGTTAAACACCCCGCCATCCCTCTTTCAAAGGGATC 370  
QY 1035 CTTTCATAGAGAACACATGAGGAGATCTTGAAGAAATTTGGATTTCAGCCGGAAGAGA 1094  
DB 371 CTTTCATAGAGAACACATGAGGAGATCTTGAAGAAATTTGGATTTCAGCCGGAAGAGA 430  
QY 1095 TTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCTAGTCTCTAAC 1154  
DB 431 TTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCTAGTCTCTAAC 490  
QY 1155 TTCCAGGCCACGGCTCAAGTGAATTTGAATTAAGTCTGATTTACAGTGTAGAGTAACACATA 1214  
DB 491 TTCCAGGCCACGGCTCAAGTGAATTTGAATTAAGTCTGATTTACAGTGTAGAGTAACACATA 550  
QY 1215 ACATTGTATGATGGAACATGAGGAACAGTATTAACAGTCTTACCACTCTTAATCAAG 1274  
DB 551 ACATTGTATGATGGAACATGAGGAACAGTATTAACAGTCTTACCACTCTTAATCAAG 610  
QY 1275 AAAAGAAATACAGACTCTGATCTTACAGATGATTTGAATTTCTAAATGTTTATCATTTA 1334  
DB 611 AAAAGAAATACAGACTCTGATCTTACAGATGATTTGAATTTCTAAATGTTTATCATTTA 670  
QY 1335 GGGCTTTTGATTTATAAAACTTTGGTACTTATA-CTAAATATGTTAGTATTTCTGCT 1393  
DB 671 GGGCTTTTGATTTATAAAACTTTGGTACTTATACTTAACTATATGTTAGTATTTCTGCT 730  
QY 1394 TCCAGTTTCCTGATATATTTGTTGATATTAAGATTTCTTGAATTTATTTGAATGGGTT 1453  
DB 731 TCCAGTTTCCTGATATATTTGTTGATATTAAGATTTCTTGAATTTATTTGATTTG-ATGGGTT 789  
QY 1454 CTAGTGAAGAAAGGATGATATTTCTTGAAGACATGATATACATTTATTTACCTCTTG 1513  
DB 790 CTAGTGAAGAAAGGATGATTTATTTCTTGAAGACATTTGATTTATTTTAACTTTCTTG 849  
QY 1514 ATTCTACAAATGTAGAAAT--GAGGAAATGCCACAAATG--TATGGTATATAAG 1565  
DB 850 ATTCTACAAATGTAGAAATTTGAGGAAATGCCCAATTTGGTTATGTTGATATAAG 905

RESULT 11  
US-11-266-748A-84584  
; Sequence 84584, Application US/11266748A

; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 84584  
; LENGTH: 924  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (773)..(773)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (822)..(822)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (903)..(903)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-84584

Query Match 45.3%; Score 734.6; DB 8; Length 924;  
Best Local Similarity 97.7%; Pred. No. 8.3e-133;  
Matches 798; Conservative 0; Mismatches 14; Indels 5; Gaps 5;

QY 719 CAGTCTTACGAGCTCTGATCAAGGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAG 778  
DB 1 CAGTCTTACGAGCTCTGATCAAGGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAG 59  
QY 779 ATGACATGATGATTTGCCAGAAATGAAGAGATTTGAGATGATTTGCAAGAG 838  
DB 60 ATGACATGATGATTTGCCAGAAATGAAGAGATTTGAGATGATTTGCAAGAG 119  
QY 839 ACGAGGACAGATGCTGTCATATCTTTGACCGCACAGATGCTGTCGACTCCGTTCTG 898  
DB 120 ACGAGGACAGATGCTGTCATATCTTTGACCGCACAGATGCTGTCGACTCCGTTCTG 179  
QY 899 ACTTTTGAGGAGTGTGTCATCATGATCAACAGGAACGGGGCTCGTTTATCACCAGT 958  
DB 180 ACTTTTGAGGAGTGTGTCATCATGATCAACAGGAACGGGGCTCGTTTATCACCAGT 239  
QY 959 GAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCT 1018  
DB 240 GAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCT 299



QY 1496 CATTATTACACTCTT-GATTCTACAATGTAGAAAA 1531  
|||||  
Db 780 CATTATTACACTCTTGGATCTACAATGGTAGAAA 816  
|||||

RESULT 13  
US-11-266-748A-137395/c  
; Sequence 137395, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 137395  
; LENGTH: 924  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (22)..(22)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (52)..(52)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (103)..(103)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (152)..(152)  
; OTHER INFORMATION: n is a, c, g, or t  
; US-11-266-748A-137395

Query Match 45.3%; Score 734.6; DB 8; Length 924;  
Best Local Similarity 97.7%; Pred. No. 8.3e-133;  
Matches 798; Conservative 0; Mismatches 14; Indels 5; Gaps 5;  
QY 719 CAGTTCTACAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATCTCCCAATCAG 778  
Db 924 CAGTTTACAGCTGTTGA-CAAAGGCACTGGACTAAAGTCTGATGACCTTCCAATCCAG 866  
QY 779 ATGAGCATGATGATGGCCAGAAATCAAGAGAAAGTTTCAGATGATTTTCAAGAGAG 838  
Db 865 ATGAGCATGATGATGGCCAGAAATCAAGAGAAAGTTTTCAGATGATTTTCAAGAGAG 806  
QY 839 ACGAAGGCAAGTGGTGTCAAAATCTTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCG 898  
|||||

Db 805 ACGAAGCCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCG 746  
QY 899 ACTTTTGGAGGAGTTGTTTCATCATGATCACAACAAGGAAACGGGGCTCGTTTATCACCAGT 958  
Db 745 ACTTTTGGAGGAGTTGTTTCATCATGATCACAACAAGGAAACGGGGCTCGTTTATCACCAGT 686  
QY 959 GAGGAGCAGGAGCGTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCT 1018  
Db 685 GAGGAGCAGGAGCGTGAGCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCT 626  
QY 1019 TCTTTCAAAGGGATCCTTTTATAGAGAAACACACATGAGGAGATACTTGAAGAATTTGA 1078  
Db 625 TCTTTCAAAGGGATCCTTTTATAGAGAAACACACATGAGGAGATACTTGAAGAATTTGA 566  
QY 1079 TTCAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAGGTA 1138  
Db 565 TTCAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAGGTA 506  
QY 1139 AAAGCTAGTCTCTAACTTCCAGGGCCACGGCTC- AAGTGAATTTGAATACTGCATTTACA 1197  
Db 505 AAAGCTAGTCTCTAACTTCCAGGGCCACGGCTCAAAGTGAATTTGAATACTGCATTTACA 446  
QY 1198 GTGTAGAGTAACACATAACATTTGATGATGGAACATGGAGGAACAGTATTACAGTGTCT 1257  
Db 445 GTGTAGAGTAACACATAACATTTGATGATGGAACATGGAGGAACAGTATTACAGTGTCT 386  
QY 1258 CTACCACCTTAATCAAGAAAGAAATTCAGACTCTGATTTCTACAGTGATGATTGAATCT 1317  
Db 385 CTACCACCTTAATCAAGAAAGAAATTCAGACTCTGATTTCTACAGTGATGATTGAATCT 326  
QY 1318 AAAAATGGTTATCATTAGGGCTTTTGAATTTATAAAAATTTGGGTACTTATATAAATAT 1377  
Db 325 AAAAATGGTTATCATTAGGGCTTTTGAATTTATAAAAATTTGGGTACTTATATAAATAT 266  
QY 1378 GGTAGTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATATAAGATTTCTTGACTT 1437  
Db 265 GGTAGTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATATAAGATTTCTTGACTT 206  
QY 1438 ATATTTTGAATGGGTTCTAGTGAAAGAAAGATGATATATTCTTGAAGACATC-GATATA 1495  
Db 205 ATATTTTGAATGGGTTCTAGTGAAAGAAAGATGATATATTCTTGAAGACATCNGATATA 146  
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RESULT 14  
US-11-344-932-74  
; Sequence 74, Application US/11344932  
; Publication No. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota



```
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; PRIOR FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 317, 430
; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-74
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Best Local Similarity 98.5%; Pred. No. 2.1e-90;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Qy 1096 TTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTCTAACT 1155
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Qy 1156 TCCAGGCCACCGCTCAAGTGAATTTGAATCTAGTCAATTTACAGTGTAGTAACACATAA 1215
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Qy 1276 AAAGAATTTACAGACTCTGATTTCTACAGTGTGATTTCTAAATTTCTAAAAATGGTTATCATTAG 1335
Db 241 AAAGAATTTACAGACTCTGATTTCTACAGTGTGATTTCTAAATTTCTAAAAATGGTTATCATTAG 300

Qy 1336 GGCCTTTGATTTATAAACTTTGGGTACTTATCTAAATATGTTAGTTATTCGCCCTTC 1395
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Qy 1516 TCTACAAATGTAGAAAATG-AGGAAATGCCACAAATTTGTATGGTGATATAAAAGTCACGT 1571
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RESULT 15
US-11-349-541-74
; Sequence 74, Application US/11349541
; Publication No. US20060223129A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C7
; CURRENT APPLICATION NUMBER: US/11/349,541
; CURRENT FILING DATE: 2006-02-06
; PRIOR APPLICATION NUMBER: US 09/116,134
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,606
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US 09/020,747
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 08/904,809
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/806,596
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(537)
; OTHER INFORMATION: n = A,T,C or G
US-11-349-541-74
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Query Match 31.8%; Score 515; DB 10; Length 537;
Best Local Similarity 98.5%; Pred. No. 2.1e-90;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1036 TTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGCCGCGAAGAGAT 1095
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Qy 1096 TTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTCTAACT 1155
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Qy 1396 CAGTTTGGCTTGATATATTGTTGATTAAGAAATCTTGACTTATATTGTAATGGGTTCT 1455
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Db	361	CAGTTTCCTTGGATATATTGTTGGATATAAGATTC TTGACTTATATTTTGAAATGGGTCTT	420
Qy	1456	AGTGAAAAAAGGAATGATATATCTTCTGAAGACATCGATATACATTTATTTTACACTCTTGAT	1515
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Qy	1516	TCTACAATGTGAAAAATG-AGGAAAATGCCCAAAATTTGTATGGTGATATAAAAGTCACGT	1571
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Job time : 561.33 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:14:13 ; Search time 12993.5 Seconds  
(without alignments)  
6976.201 Million cell updates/sec

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Perfect score: 1621  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues  
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1571	96.9	1967	6	CR625004 full-leng
2	1571	96.9	3111	6	CR616479 full-leng
3	1532.6	94.5	1544	6	CR615811 full-leng
4	1455.6	89.8	1598	6	CR618063 full-leng
5	1367.8	84.4	1606	6	CR857309 Pongo pyg
6	935.2	57.7	1042	4	BX359836 BX359836
7	916.4	56.5	977	1	AL558928 AL558928
8	915.6	56.5	1534	6	AY609940 Sus scrofa
9	887.6	54.8	924	4	BX449004 BX449004
10	882.2	54.4	971	1	AL571115 AL571115
11	863	53.2	1081	1	AL545355 AL545355
12	848.8	52.4	955	2	BG741165 602631843
13	845.8	52.2	1076	1	AL555978 AL555978
14	822.2	50.7	990	1	AL551698 AL551698
15	813.6	50.2	823	3	BM723657 UI-E-EJ0-
16	807.4	49.8	1523	6	AK002401 Mus muscu
17	807.4	49.8	2576	6	AK048249 Mus muscu
18	801	49.4	1558	6	AK160586 Mus muscu
19	794.4	49.0	893	1	AL558977 AL558977

20 783 48.3 958 4 BX390793  
21 747 46.1 890 3 BQ962523 AGENCOURT  
22 735 45.3 871 4 BX449005 BX449005  
23 733.4 45.2 805 5 CD643323 AGENCOURT  
24 727.8 44.9 790 8 CR856058 DKF2p469P  
25 726.4 44.8 890 3 BQ941482 AGENCOURT  
26 719 44.4 808 2 B1256255 602975075  
27 708.6 43.7 740 3 BM675180 UI-E-EJ0-  
28 693.8 42.8 880 2 BG289921 602381336  
29 684.4 42.2 712 1 A1796120 wh42f03.x  
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33 664.6 41.0 943 2 BG289079 602383954  
34 660.8 40.8 687 1 A1373634 qz53d12.x  
35 660 40.7 812 2 BG035606 602325670  
36 658.6 40.6 790 8 CR764669 DKF2p469K  
37 657.2 40.5 754 8 CR764668 DKF2p469K  
38 654.2 40.4 693 2 BG779839 602667316  
39 653.8 40.3 870 8 CO880994 BovGen.09  
40 646.6 39.9 821 10 DR774055 ILUMIGEN  
41 642.4 39.6 654 7 AW271287 xs46a08.x  
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## ALIGNMENTS

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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REMARK  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
ORIGIN

1967 bp mRNA linear HTC 21-JUL-2004  
full-length cDNA clone CS0DJ007YI07 of T cells (Jurkat cell line)  
Cot 10-normalized of Homo sapiens (human).  
CR625004.1 GI:50505811  
HTC; CDSLT cDNA.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 1967)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization.  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1967)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
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Best Local Similarity		99.7%; Pred. No. 0;
Matches 1574; Conservative		0; Mismatches 5; Indels 0; Gaps 0;
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Qy	121	CCGCTACGACGTGAGCGCTTGGCGCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180
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Qy	181	CGCCGGGGAGCGCGCTGTCGCGCGCTCTGTCAAGCGGTCCGATGTGCTGTGGAGCC 240
Db	221	CGCCGGGGAGCGCGCTGTCGCGCGCTCTGTCAAGCGGTCCGATGTGCTGTGGAGCC 280
Qy	241	CTTCCGCGCGGTGTATGAGAACTCCAGCTGGGCCAGAGATTCGCAAGCGGAAAA 300
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Qy	301	TCCAAGGCTTATGTCAGGCTGAGTGGATTTGGCCAGTCAGAGCTTCTGCCGGTT 360
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Db	641	GAATTCGAGTCTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGGTGAGCACCTTT 700
Qy	661	CTATACGACTTACAGGACAGCATGCGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
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Qy	781	GAGCATGATGATTTGGCCAGAAATGAAGAAAGTTTCAGATGATTTTGAAGAAAGAC 840
Db	821	GAGCATGATGATTTGGCCAGAAATGAAGAAAGTTTTCAGATGATTTTGAAGAAAGAC 880
Qy	841	GAAGCAGAGTGGTGTCAAACTTTTGAACGACAGATGCTGTGTGACTCCGGTCTGAC 900
Db	881	GAAGCAGAGTGGTGTCAAACTTTTGAACGACAGATGCTGTGTGACTCCGGTCTGAC 940
Qy	901	TTTTGAGGAGGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
Db	941	TTTTGAGGAGGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 1000
Qy	961	GGAGCAGAGCTGAGCCCGCCCTGACCTCTGTGTAAACACCCCGAGCATCCCTTC 1020
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Qy	1081	CAGCCGGAAGAGATTATTAATCAGCTTAACCTCAGATAAAATCAATTTGAAAGTAATAGGTAAA 1140
Db	1121	CAGCCGGAAGAGATTATTAATCAGCTTAACCTCAGATAAAATCAATTTGAAAGTAATAGGTAAA 1180
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Db	1181	AGCTAGTCTTAATCTCCAGGCCACCGCTCAAGTGAATTTTGAATCTACTGCAATTTACAGTG 1240
Qy	1201	TAGAGTAACACATAAATCTATGTCATGGAACATGGAGGAACAGTATTACAGTGTCTTA 1260
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Qy	1261	CCACTCTTAATCAAGAAAGAAATTTACAGACTCTGATCTTCAAGTGAATTTGAATTTTAAA 1320
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Qy	1381	AGTTATTTCTCCCTTCCAGTTTGTGATATATTTTGTGATTTTAAAGATTTCTTGACTTATA 1440
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Qy	1441	TTTTGAATGGTTCTAGTGAAGAAAGAAATGATATATTTCTTTGAAGACATCGATATACATTT 1500
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Qy	1501	ATTACACTCTTCTGATCTACAATGTAGAAATGAGGAATGCCACAAATTTGTATGGTAT 1560
Db	1541	ATTACACTCTTCTGATCTACAATGTAGAAATGAGGAATGCCACAAATTTGTATGGTAT 1600
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LOCUS		of Homo sapiens (human) .
DEFINITION		CR616479
ACCESSION		CR616479.1 GI:50497286
VERSION		HTC; CNSLT_CDNA.
KEYWORDS		Homo sapiens (human)
SOURCE		Homo sapiens
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE		1. (bases 1 to 3111)
AUTHORS		Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE		Full-length cDNA libraries and normalization
JOURNAL		Unpublished
REMARK		Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE		2. (bases 1 to 3111)
AUTHORS		Genoscope.
TITLE		Direct Submission
JOURNAL		Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT		- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life technologies, a division of Invitrogen.
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## ORIGIN

Query Match 96.9%; Score 1571; DB 6; Length 3111;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1574; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGCAGGCGATCTCGGTCTATGAGCTGTCCGGCTCGCCCGCGGCGCGTT 60  
DB 73 CGCCATGGCACTGCAGGCGATCTCGGTCTGAGCTGTCCGGCTCGCCCGCGGCGCGTT 132  
QY 61 CTGTGCTATGCTCTGGCTGACTTTCGGGGCGGTGTGTACGGTGGACCGGCGCGGCTC 120  
DB 133 CTGTGCTATGCTCTGGCTGACTTTCGGGGCGGTGTGTACGGTGGACCGGCGCGGCTC 192  
QY 121 CGCTACGACGTGAGCGGCTTGGCGCGGCGAAGCGCTCGTAGTCTGACCTGAAGCA 180  
DB 193 CGCTACGACGTGAGCGGCTTGGCGCGGCGAAGCGCTCGTAGTCTGACCTGAAGCA 252  
QY 181 GCGCGGGGAGCGCGCTGCTCGGCGGTCTGTCAAGCGGTGCGATGCTGCTGGAGCC 240  
DB 253 GCGCGGGGAGCGCGCTGCTCGGCGGTCTGTCAAGCGGTGCGATGCTGCTGGAGCC 312  
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DB 313 CTTTCGCCCGGCTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCCTCAGCGGGA 372  
QY 301 TCCAGGCTTATTAATGCCAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGTT 360  
DB 373 TCCAGGCTTATTAATGCCAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGTT 432  
QY 361 AGCTGCCACGATATCAACTATTGGCTTTGTGAGGTCTCTCAAAAATGGCAGAAG 420  
DB 433 AGCTGCCACGATATCAACTATTGGCTTTGTGAGGTCTCTCAAAAATGGCAGAAG 492  
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DB 493 TGGTGAGATTCGATATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGGCTTAT 552  
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DB 553 GTGTGACCTGGGCAATTAATATGGCTCTTTTGAACCGCACACGCACTGAACGGTCAGT 612  
QY 541 CATTTGATCAAAATATGCTGGAAGAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCA 600  
DB 613 CATTTGATCAAAATATGCTGGAAGAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCA 672  
QY 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 660  
DB 673 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTT 732  
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DB 733 CTATACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATGAACCCCA 792  
QY 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAGTCTGATGAATCTCCCAATCAGAT 780  
DB 793 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAGTCTGATGAATCTCCCAATCAGAT 852  
QY 781 GAGCATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCCAAGAAGAC 840  
DB 853 GAGCATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCCAAGAAGAC 912  
QY 841 GAAGGACAGATGGTGTCAAAATCTTTGACGCGACAGATGCTGTGACCTCCGTTCTGAC 900  
DB 913 GAAGGACAGATGGTGTCAAAATCTTTGACGCGACAGATGCTGTGACCTCCGTTCTGAC 972  
QY 901 TTTTGAGGAGGTGTTTCATCATCATCAACAAGGAACGGGGCTCGTTTTATCACCAGTGA 960

DB 973 TTTTGAGGAGGTGTTTCATCATGATCAACAAGGAACGGGCTCGTTTTATCACCAGTGA 1032  
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DB 1033 GGAGCAGGACGTGAGCCCGCCCTGCACTCTGCTGTAAACACCCAGCCATCCCTTC 1092  
QY 1021 TTTTCAAAAGGATCCCTTTTCATAGGAGAACACACCTGAGGAGATCTTTGAAGAAATTTGGATT 1080  
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QY 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATGAAGTAAA 1140  
DB 1153 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATGAAGTAAA 1212  
QY 1141 AGCTAGTCTCTTAACCTTCCAGGCCCGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200  
DB 1213 AGCTAGTCTCTTAACCTTCCAGGCCCGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1272  
QY 1201 TAGAGTAAACATAAATTTGATGATGGAACATGGAGAACAGTATTACAGTGTCTTA 1260  
DB 1273 TAGAGTAAACATAAATTTGATGATGGAACATGGAGAACAGTATTACAGTGTCTTA 1332  
QY 1261 CCACCTCTAATCAAGAAAAGATTTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1320  
DB 1333 CCACCTCTAATCAAGAAAAGATTTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1392  
QY 1321 AATGGTATCATTAGGGCTTTTGATTTATAAACTTTGGGTACTTATCTAAATTTATGCT 1380  
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QY 1381 AGTTATCTGCCCTCCAGTTTGTGATATTTTGTGATATAATTAAGATTTCTTGACTTATA 1440  
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QY 1441 TTTTGAATGGTCTTAGTGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500  
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DB 1573 ATTTACACTCTGATCTTACATGTAGAAATGAGAAATGAGAAATGAGAAATGAGTATGAT 1632  
QY 1561 AAAAGTCACTGGAACAAA 1579  
DB 1633 AAAAGTCACTGGAACAAA 1651

## RESULT 3

CS615811

LOCUS

DEFINITION

1544 bp mRNA linear HTC 21-JUL-2004  
full-length cDNA clone CS0D1027YJ12 of Placenta Cot 25-normalized  
of Homo sapiens (human).

ACCESSION

CR615811

VERSION

CR615811.1 GI:50496618

KEYWORDS

HTC; CDS; cDNA.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1544)

Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paradise Avenue

2 (bases 1 to 1544)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

## ORIGIN

Query Match	94.5%	Score 1532.6	DB 6	Length 1544
Best Local Similarity	99.7%	Mism. No. 0		
Matches 1535	Conservative	0	Indels	0
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Db	6	CGCCATGGCACTGCAGGCGCATCTCGGTTCGTGTAGAGCTGTCCGGCCCTGGCCCGGGGCCCGGTT	65	
Qy	61	CTGTGCTATGTTCCTGGCTGACTTCGGGGCGCGTGTGTATCGCTGTGAGCCCGGCCCGGCTC	120	
Db	66	CTGTGCTATGTTCCTGGCTGACTTCGGGGCGCGTGTGTATCGCTGTGAGCCCGGCCCGGCTC	125	
Qy	121	CCGCTACGACGTGAGCCCTTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTCAAGCA	180	
Db	126	CCGCTACGACGTGAGCCCTTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTCAAGCA	185	
Qy	181	GCCGCGGGAGCGCGCTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTCTCGAGCC	240	
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Qy	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAGAG	420	
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Db	426	TGSGTGAAGTCCGTATGCCCGCTCAATCTCCTGCTGACTTTGCTGGTGGTGGGCTTAT	485	
Qy	481	GTGTGCACTGGGCATTAAATGGCTCTTTTTCACCGCACACGCACTGACAAAGGTCAGGT	540	
Db	486	GTGTGCACTGGGCATTAAATGGCTCTTTTTCACCGCACACGCACTGCGCAAGGTCAGGT	545	
Qy	541	CATTGATGCAATATGTTGGGAAGGAACAGCATATTTAAGTCTCTTTCTGTGAAAACTCA	600	
Db	546	CATTGATGCAATATGTTGGGAAGGAACAGCATATTTAAGTCTCTTTCTGTGAAAACTCA	605	
Qy	601	GAATTCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT	660	
Db	606	GAATTCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT	665	
Qy	661	CTATACGACTTACAGGACAGAGATGGGAAATTCATGCTGTTGGAGCAATAGAAACCCCA	720	
Db	666	CTATACGACTTACAGGACAGAGATGGGAAATTCATGCTGTTGGAGCAATAGAAACCCCA	725	
Qy	721	GTTCTTACAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT	780	
Db	726	GTTCTTACAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT	785	
Qy	781	GAGCATGATGATTTGGCCCAAGAAATCAAGAAAGATTTTGAGATGATTTATTTGCAAGAGAC	840	

AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
COMMENT - Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="CS0DM013V103"  
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Best Local Similarity 96.9%; Pred. No. 8.2e-313; Indels 45; Gaps 1;  
Matches 1513; Conservative 0; Mismatches 4;  
QY 1 CGCCATGGCACTGCAGGCGATCTCGGTTCATGAGCTGTCCGGCTCGGCCCGGCGCGTT 60  
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QY 61 CTGTGCTATGGTCTCGGTGACTTTCGGGGCGCTGTGTGTAACGGTGAACCGGCCCGGCTC 120  
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QY 181 GCCCGGGGAGCGCGCTGTGCGGGCTGTGTCAAGCGGTCCGATGTGCTGCGAGCC 240  
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QY 241 CTTTCGCGCGGTGTCTATGAGAAATCCAGCTGGGCGGAGAGATTCGAGCGGGAAAA 300  
DB 322 CTTTCGCGCGGTGTCTATGAGAAATCCAGCTGGGCGGAGAGATTCGAGCGGGAAAA 381  
QY 301 TCCAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGTT 360  
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QY 361 AGCTGCCACATATCAACTATTTGGCTTTGTGAGGTTCTCTCAAAAATGGCAGAAAG 420  
DB 442 AGCTGCCACATATCAACTATTTGGCTTTGTGAGGTTCTCTCAAAAATGGCAGAAAG 501  
QY 421 TGTGAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGGCTTAT 480  
DB 502 TGTGAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGGCTTAT 561  
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QY 661 CTATAGCACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATGAACCCCA 720  
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QY 721 GTTCTACGAGCTCTGATCAAGGACTTGGAGCTAAAGTCTGATGAACCTCCCAATCAGAT 780

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QY 901 TTTTGAAGAGTGTGTCTCAATCATCATGATCAAAAGGAAACGGGGCTCTGTTATCACAGTGA 960  
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DB 1357 AATGGTTATCATAGGGCTTTTGATTTATAAACTTTGGGTACTTATCTAAATTTATGTT 1416  
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QY 1561 AA 1562  
DB 1597 AA 1598  
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CR857309  
LOCUS Pongo pygmaeus mRNA; cDNA DKFp469O1232 (from clone DKFp469O1232).  
DEFINITION  
ACCESSION CR857309  
VERSION CR857309.1 GI:55725646  
KEYWORDS HTC.  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Pongo.  
REFERENCE 1 (bases 1 to 1606)







division of Invitrogen. This sequence belongs to sequence cluster 2801.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?c=CS0DJO07AE04QP1&c=2801.r>.

## FEATURES

source

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/mol_type="mrna"
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## ORIGIN

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Query Match      56.5%; Score 916.4; DB 1; Length 977;
Best Local Similarity 99.4%; Pred. No. 6.6e-193;
Matches 928; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

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Qy 121 CGCTACGACGTGACCGCTTGGGGCGGGGCAAGCGCTCGTGTGCTGGACCTGAAGCA 180
Db 161 CGCTACGACGTGACCGCTTGGGGCGGGGCAAGCGCTCGTGTGCTGGACCTGAAGCA 220

Qy 181 GCCCGGGGAGCGCGCTGCTCGCGCTGTGTGCAAGCGGTGCGATGCTGTGCGAGCC 240
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Qy 301 TCCAAAGGCTTATTTATGCCAGGCTCAGTGGATTTCGCCAGTCAGAACTTCTGCCGTT 360
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Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAG 420
Db 401 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAG 460

Qy 421 TGGTGAGAACTCGATATGCCCGCTCAATCTCTGCTGACTTTGCTGGTGGTGGCTTTAT 480
Db 461 TGGTGAGAACTCGATATGCCCGCTCAATCTCTGCTGACTTTGCTGGTGGTGGCTTTAT 520

Qy 481 GTGTGACCTGGGCATTATAATGGCTCTTTTGGACCGCACAGCATGACAGGGTCAGGT 540
Db 521 GTGTGACCTGGGCATTATAATGGCTCTTTTGGACCGCACAGCATGACAGGGTCAGGT 580

Qy 541 CATTGATGCAATATGGTGGAGGACAGCATATTTAAGTTCTTTCTGTGGAACATCA 600
Db 581 CATTGATGCAATATGGTGGAGGACAGCATATTTAAGTTCTTTCTGTGGAACATCA 640

Qy 601 GAAATCGAGTCTGTGGAGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660
Db 641 GAAATCGAGTCTGTGGAGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 700

Qy 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 720
Db 701 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 760

Qy 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTCCTCCAAATCAGAT 780
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Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAAGATTTGCGAGATGATTTGCAAGAAAGAC 840
Db 821 GAGCATGGATGATGGCCAGAAATGAAGAAAGATTTGCGAGATGATTTGCAAGAAAGAC 880
Qy 841 GAAGGACAGTGTGTCAAAATCTTTGACGGCAGATGCGCTGTGACTCCGGTTCGTGAC 900
Db 881 G-ARGSAGATGGTGTCAAAATCTTTGACGGCAGATGCGCTGTGACTCCGGTTCGTGAC 939
Qy 901 TTTTGACGAGTGTTCATCATGATCACAACAAG 934
Db 940 TTTTGACGAGTGTTCATCATGATCACAACAAG 973

RESULT 8
AV609940
LOCUS AV609940 1534 bp mRNA linear HTC 31-JAN-2005
DEFINITION Sus scrofa clone Clu_4587.scr.msk.pl.Contigl, mRNA sequence.
ACCESSION AY609940
VERSION AY609940.1 GI:52351510
KEYWORDS HTC.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 1534)
AUTHORS Jorgensen,F.G., Hobolth,A., Hornshoj,H., Bendixen,C., Fredholm,M.
and Schierup,M.H.
TITLE Comparative analysis of protein coding sequences from human, mouse
and the domesticated pig
JOURNAL (er) BMC Biol. 3 (1), 2 (2005)
PUBMED 15679890
REFERENCE 2 (bases 1 to 1534)
AUTHORS Hornshoj,H., Bendixen,C. and Panitz,F.
TITLE Direct Submission
JOURNAL Submitted (28-APR-2004) Animal Breeding and Genetics, Danish
Institute of Agricultural Sciences, Research Centre Foulum, Postbox
50, Tjele DK-8830, Denmark
FEATURES
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Matches 1137; Conservative 0; Mismatches 259; Indels 26; Gaps 4;

Qy 1 CGCCATGGCACTCAGGGGCACTCTCGGTATGAGAGCTGTCCGGCTCGGCCCGGCCCGTT 60
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Qy 61 CTGTGCTATGGTCTGTGGCTGACTTTCGGGGCGGCTGTGTTAGCTGAGCCCGCCGGCTC 120
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Qy 181 GCCCGGGGAGCCCGCGGTGCTGTGCAAGCGGTGCGATGCTGTGAGGCC 240
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DB	384	TCCAAAGCTTATCTACGCGAGGCTGAGTGGTTTTGGCCAGTCAGGAAGATCTCTTCAAGT	443
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DB	804	GTTCTATGAGCTGCTGTTCAAGGACTCGGACTAAAGTCTGATGAACTTCCCAATCAGAT	863
QY	781	GAGCATGGATGATTTGGCCAGAAATGAAGAAGAGTTTTCAGATGATTTTGCAAAAGAGAC	840
DB	864	GAGCATAAAGGATTTGGCCAGAAATGAAGAAGAAATTTTCAGATGATTTTGCAAAAGAGAC	923
QY	841	GAAGGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCGGTTCTTGAC	900
DB	924	AAAGGCAGAGTGGTGTGAGATCTTCGATGGCACAGATGCAATGTGTGACTCTCTGTTCTGAC	983
QY	901	TTTGTGAGAGGTTGTTTCATCATGATCAACAAGGAAACGGGGCTCGTTTATCACAGTGA	960
DB	984	TCGTGAAGAGTTGCGCATCATGGTCATACAAAGATCGGGGCTCATTTATTACTGACGG	1043
QY	961	GGAGCAGGACGTGAGCCCCCGCTGCACCTCTGCTGTAAACACCCAGCCCATCCCTTC	1020
DB	1044	GGAGCAGGCTGTGAGTCCCCCGCTGCACCTCTCTCCTCAACACCCAGCCGCTCCCATC	1103
QY	1021	TTTCAAAAGGATTCCTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGATT	1080
DB	1104	CTCTGAAGAGAAATCCCTTTGTAGGAGAAACATACAGAAAGATACCTTAAAGAAATTTGGGTT	1163
QY	1081	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAAGTAAATAGGTA	1140
DB	1164	CAGCCAGGAAGAGATCATTCAGCTTAAAGTCTGATGAATTTATTGAAAGTAAATACCAAG	1223
QY	1141	AGCTAGTCTCTAA-----CTTCCAGGCCCCAGGCTCAAGTGAATTTGAAATACGTGCAT	1192
DB	1224	ATCTAAGATCTAATCTCTAAGTTCCAGGTTCCAACTCAAGTGAATTTGAGTATTCAT	1283
QY	1193	TTACAGTGTAGAGTAACACA--TAACTATTGTATGATGGAAACATGGAAGAACAGTATTAC	1251
DB	1284	TTACAGTATAGTGTAAATGCGAAAAAATCGTATGATAGAAAAACGAGAAAAACAATATCAC	1343
QY	1252	AGTGTCTCTACCATCTCAATCAAGAAAGAAATTACAGACTCTGATTCTACAGTGAATG	1311
DB	1344	AGTGGTCCAGCTATTTCTAATTCAGAAACA-----AGATTTCTGCTTATACAGTAAATGATCG	1398
QY	1312	AACTTTAAAAATGGTGTATCATATAGGCGCTTTTGATTTATAAAACTTTGGGTACTTATACTA	1371

[illegible]

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QY 887 ACTCCGGTCTGACCTTTGAGAGAGTGTGTCATCATGATCACAACAGAAACGGGCTCG 946
Db 675 ACTCCGGTCTGACCTTTGAGAGAGTGTGTCATCATGATCACAACAGAAACGGGCTCG 616
QY 947 TTTATCACAGTGAGGAGCAGGACGTGAGCCGCCCTGACCTCTGCTGTGTAACACC 1006
Db 615 TTTATCACAGTGAGGAGCAGGACGTGAGCCGCCCTGACCTCTGCTGTGTAACACC 556
QY 1007 CCAGCCATCCCTTTCTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTT 1066
Db 555 CCAGCCATCCCTTTCTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTT 496
QY 1067 GAAGAAATTTGGATTGAGCGCGAAGAGATTTATCAGCTTAATCAGATAAAATCATTTGAA 1126
Db 495 GAAGAAATTTGGATTGAGCGCGAAGAGATTTATCAGCTTTGATCAGATAAAATCATTTGAA 436
QY 1127 AGTAATAAGGTAAGGTAAGCTAGTCTCTAACTCCAGGCCCCAGGCTCAAGTGAATTTGAATA 1186
Db 435 AGTAATAAGGTAAGGTAAGCTAGTCTCTAACTCCAGGCCCCAGGCTCAAGTGAATTTGAATA 376
QY 1187 CTGCATTTTACAGTGTAGAGTAACACATAACATTTGTATGTCATGGAACATGAGGAAACAGT 1246
Db 375 CTGCATTTTACAGTGTAGAGTAACACATAACATTTGTATGTCATGGAACATGAGGAAACAGT 316
QY 1247 ATTACAGTGTCTTACACTCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTAT 1306
Db 315 ATTACAGTGTCTTACACTCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTAT 256
QY 1307 GATTCGAATTTCTAAAATGCTTATCATTTAGGCGCTTTTGATTTTATAAACTTTGGGTACTTA 1366
Db 255 GATTCGAATTTCTAAAATGCTTATCATTTAGGCGCTTTTGATTTTATAAACTTTGGGTACTTA 196
QY 1367 TACTAAATTTAGTGTAGTATTTCTGCTTCCAGTTTCTGTATGATATATTTGTTGATTTAAG 1426
Db 195 TACTAAATTTAGTGTAGTATTTCTGCTTCCAGTTTCTGTATGATATTTGTTGATTTAAG 136
QY 1427 ATTCCTGTGATTTATTTGAAATGGGTTCTAGTGAAAGAAAGAAATGATATTTCTTGAAGAC 1486
Db 135 ATTCCTGTGATTTATTTGAAATGGGTTCTAGTGAAAGAAAGAAATGATATTTCTTGAAGAC 76
QY 1487 ATCGATATACATTTATTTACACTCTTGATTTCTACAAATGTAGAAAATGAGGAAATGCCACA 1546
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QY 1547 AATTGTATG 1555
Db 15 AATTNNATB 7
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RESULT 10
AL571115/c
LOCUS
DEFINITION
AL571115 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Clone CS0D1027YJ12 3-PRIME, mRNA sequence.
AL571115
VERSION
AL571115.3 GI:46237222
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 971)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31292520.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2801.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?s=CS0D1027DE06NP1&c=2801.r>.

## FEATURES

source

Location/Qualifiers

1..971

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D1027YJ12"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

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Query Match 54.4%; Score 882.2; DB 1; Length 971;
Best Local Similarity 96.3%; Pred. No. 2.7e-185;
Matches 893; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

QY 612 TGTGGGAGCACCCTCGAGGACAGACATGTTGGATGCTGGGACACCTTCTATACGACTT 671
Db 926 YGTGTGAACCCCTCGRMGACAGGACATGTGANTGGT-GRGCACCTTTTCAWAACTA 868
QY 672 ACAGCAGCAGCAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTCCTACGAGC 731
Db 867 ACAGAACAGAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTCCTACGAGC 808
QY 732 TGCTGATCAAGGACTTTGGACTTAAATCTGATGAATCCCAATCAGATGAGCATGGATG 791
Db 807 TGCTGATCAAGGACTTTGGACTTAAATCTGATGAATCCCAATCAGATGAGCATGGATG 748
QY 792 ATTGCCAGAAATCAAGAGAAAGTTTCAGATGTTTTCGAAAGAACGAGCAGAGT 851
Db 747 ATTGCCAGAAATCAAGAGAAAGTTTCAGATGTTTTCGAAAGAACGAGCAGAGT 688
QY 852 GGTGTCAAACTTTTGACGGCAGCAGATGCTGTGATCTCGGTTCTGACTTTTGAGGAGG 911
Db 687 GGTGTCAAACTTTTGACGGCAGCAGATGCTGTGATCTCGGTTCTGACTTTTGAGGAGG 628
QY 912 TTGTTTCATGATGATCAACAAGGAAACGGGCTCGTTTATCACCAGTGAGGAGCAGACG 971
Db 627 TTGTTTCATGATGATCAACAAGGAAACGGGCTCGTTTATCACCAGTGAGGAGCAGACG 568
QY 972 TGAGCCCCCGCCCTGACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTCAAAAGGG 1031
Db 567 TGAGCCCCCGCCCTGACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTCAAAAGGG 508
QY 1032 ATCTCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGCCGCGAAG 1091
Db 507 ATCTCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGCCGCGAAG 448
QY 1092 AGATTTATCAGCTTTAATCAGATAAAATCAATTGAAAGTAATTAAGGTAAAGCTAGTCTCT 1151
Db 447 AGATTTATCAGCTTTAATCAGATAAAATCAATTGAAAGTAATTAAGGTAAAGCTAGTCTCT 388
QY 1152 AACTTTCAGGCCACCGCTCAAGTGAATTTGAATCTGCAATTTTACAGTGTAGAGTAAACAC 1211
Db 387 AACTTTCAGGCCACCGCTCAAGTGAATTTGAATCTGCAATTTTACAGTGTAGAGTAAACAC 328
QY 1212 ATAACATTTGATGATCGAAGAACATGAGGAAACAGTATTACAGTGTCTTACCACCTCTAATC 1271
Db 327 ATAACATTTGATGATCGAAGAACATGAGGAAACAGTATTACAGTGTCTTACCACCTCTAATC 268
QY 1272 AAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAAAATGGTTATCA 1331
Db 267 AAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAAAATGGTTATCA 208
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QY 1332 TTAGGCGCTTTGATTTATATAAACTTTGGGTACTTATACATAAATATGGTAGTATTCTGC 1391  
 Db 207 TTAGGCGCTTTGATTTATATAAACTTTGGGTACTTATACATAAATATGGTAGTATTCTGC 148  
 QY 1392 CTTCCAGTTTGGCTTGATATATTTGATATTAAGATTCTTGACATTATATTTTGAATGG 1451  
 Db 147 CTTCCAGTTTGGCTTGATATATTTGATATTAAGATTCTTGACATTATATTTTGAATGG 88  
 QY 1452 TTCTAGTGAAGAAGGAATGATATATTTCTTGAAGACATCGATATACATTTATTTACACTCT 1511  
 Db 87 TTCTAGTGAAGAAGGAATGATATATTTCTTGAAGACATCGATATACATTTATTTNACACTCT 28  
 QY 1512 TGATTTCAATGTAGAAAATGAGAA 1538  
 Db 27 NGANNCTACAATGTAGAAAACGGA 1

RESULT 11  
 AL545355  
 LOCUS  
 DEFINITION AL545355 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CS0D1027YJ12 5-PRIME, mRNA sequence.  
 ACCESSION AL545355  
 VERSION AL545355.3 GI:45745838  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:31267191.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 2801.r  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?s=CS0D1027DE06QP1&c=2801.r.

FEATURES  
 source  
 Location/Qualifiers  
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 /clone="CS0D1027YJ12"  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 53.2%; Score 863; DB 1; Length 1081;  
 Best Local Similarity 92.3%; Pred. No. 5.1e-181;  
 Matches 939; Conservative 28; Mismatches 44; Indels 6; Gaps 6;  
 QY 1 CGCCATGGCAGTCGAGGCGATCTCGGTCAATGAGCTGTCCGGCTCGGCCCGGGCCGGT 60  
 Db 6 CGCCATGGCAGTCGAGGCGATCTCGGTCTGTGAGCTGTCCGGCTCGGCCCGGGCCGGT 65  
 QY 61 CTGTGCTATGCTCTGGCTGACTTTCGGGGCGGTGTGGTACCGGTGGACCGGCCGGCTC 120  
 Db 66 CTGTGCTATGCTCTGGCTGACTTTCGGGGCGGTGTGGTACCGGTGGACCGGCCGGCTC 125

QY 121 CCGTACGACGTCGAGCCCGCTTTGGGCGGCGCAAGCGCTCGCTAGTGTGACCTGAAGCA 180  
 Db 126 CCGCTACGACGTCGAGCCCGCTTTGGGCGGCGCAAGCGCTCGCTAGTGTGACCTGAAGCA 185  
 QY 181 GCGCGGGGAGCGCGCGCTGCTGCGGCGCTCTGTGCAAGCGGTCCGATGTGCTGCGAGCC 240  
 Db 186 GCGCGGGGAGCGCGCGCTGCTGCGGCGCTCTGTGCAAGCGGTCCGATGTGCTGCGAGCC 245  
 QY 241 CTTCCGCGCGCGGTGTCTGAGGAAACTCCAGCTGGGCGCCAGAGATTCTGCAGCGGAAAA 300  
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 QY 301 TCCAAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCGCGTT 360  
 Db 306 TCCAAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCGCGTT 365  
 QY 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTCTCTCAAAAAATTTGGCAGAAG 420  
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 QY 421 TGGTGAGAAATCCGATATGCCCGCTGAATCTCTGCTGCTGACTTTGTGCTGGTGGCTTAT 480  
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 QY 481 GTGTGCACTGGGCAATTAATAATGGCTCTTTTGAACGCGCACACGCACTGAAGGGTCAGGT 540  
 Db 486 GTGTGCACTGGGCAATTAATAATGGCTCTTTTGAACGCGCACACGCACTGAAGGGTCAGGT 545  
 QY 541 CATTGATGCAATATGTTGGAGGAGACAGCATATTTAAGTTCTTTCTGTGAGAAACTCA 600  
 Db 546 CATTGATGCAATATGTTGGAGGAGACAGCATATTTAAGTTCTTTCTGTGAGAAACTCA 605  
 QY 601 GAAATCGAGTCTGTGGGAGGACACCTTCGAGGACAGAAACATGTTGGATGTTGGAGCACCTTT 660  
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 QY 661 CTATACGACTTACAGCAGCAGAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCCA 720  
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 QY 781 GAGCATGATGATTTGGCCAGGAAATCAAGCAAGTTTCAGATGATTTTTCAGAAAGAC 840  
 Db 784 GAGCATGATGATTTGGCCAGGAAATCAAGCAAGTTTCAGATGATTTTTCAGAGAC 843  
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 Db 844 GAAGGCAGTGTGTGTAAATCTTTGACGGCACAAATGCTGTGTARCTCCGGTTCTT 903  
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 Db 904 RCTTTTTRRGGGGTGTATTAATATATATAAAAAAGGAAACGGGGTCG-TTATWACMAGT 962  
 QY 959 GAGGAGCAGGAGCTGAGCCCGCTCCACTCTGCTGTTAAACACCCAGCCATC 1015  
 Db 963 AAGGGC-GGACKTAGACCCCGCCACCCTTGTGTTAAAMCCCCCCTCCCTT 1018

RESULT 12  
 LOCUS BG741165  
 DEFINITION 602631843F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4776971 5',  
 mRNA sequence.  
 ACCESSION BG741165  
 VERSION BG741165.1 GI:14051818  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              Tissue Procurement: James Cleaver, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
              Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM10630 row: f column: 12
              High quality sequence stop: 805.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4776971"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match      52.4%; Score 848.8; DB 2; Length 955;
Best Local Similarity 95.7%; Pred. No. 7.3e-178;
Matches 894; Conservative 0; Mismatches 37; Indels 3; Gaps 2;

Qy 154 GCGCTCGCTAGTGTGGACCTGAACGACGCGGGGAGCGCGTGTGGCGGCTGTG 213
Db 1 GCGCTCGCTAGTGTGGACCTGAACGACGCGGGGAGCGCGGCTGTGGCGGCTGTG 60
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Db 61 CAAGCGGTGGAGTGTGCTGTGGAGCCCTTCGCGCGGCTGTGATGGAGAAATCCAGCT 120
Qy 274 GGGCCACAGATCTTCGACGCGGGAATCCAAAGCTTATTTATGCCAGCTGATGGATT 333
Db 121 GGGCCACAGATCTTCGACGCGGGAATCCAAAGCTTATTTATGCCAGCTGATGGATT 180
Qy 334 TGGCCAGTCAGGAAGCTTCTGCGGCTAGCTGGCCACGATATCAACTATTTGGCTTTGTC 393
Db 181 TGGCCAGTCAGGAAGCTTCTGCGGCTAGCTGGCCACGATATCAACTATTTGGCTTTGTC 240
Qy 394 AGGTGTTCTCTCAAAATTTGGCAGAAAGTGGTGAAGATCCGATATGCCCGCTGAATCTCCT 453
Db 241 AGGTGTTCTCTCAAAATTTGGCAGAAAGTGGTGAAGATCCGATATGCCCGCTGAATCTCCT 300
Qy 454 GCCTGACTTTGCTGTGTGGCTTATGTGTGCACTGGGCATTAATAATGGCTCTTTTGA 513
Db 301 GCCTGACTTTGCTGTGTGGCTTATGTGTGCACTGGGCATTAATAATGGCTCTTTTGA 360
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Db 361 CGGCACGCACTGACAGGGTTCAGTTCATTTGATCAAAATATGGTGGAGGAACAGCAT 420
Qy 574 TTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACA 633
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Qy 634 GAACATGTTGGATGTGGAGCACTTTCTATAGCACTTACAGGACAGAGATGGGAATT 693
Db 481 GAACATGTTGGATGTGGAGCACTTTCTATACGACTTACAGGACAGAGATGGGAATT 540
Qy 694 CATGCTGTGGAGCAATAGAACCCAGTTCTACAGGCTGTGATCAAAAGCACTTGGACT 753
Db 541 CATGCTGTGGAGCAATAGAACCCAGTTCTACAGGCTGTGATCAAAAGCACTTGGACT 600

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754 AAAGCTGATGAACCTCCCAATCAGATGACATGGATGATGGCCAGAAATGAGAGAA 813
Db 601 AAAGCTGATGAACCTCCCAATCAGATGACATGGATGATGGCCAGAAATGAGAGAA 660
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Qy 874 AGATGCTGTGTGACTCCGGTTCGACTTTTGAGGAGGTGTTCATCATGATCAACAACAA 933
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Qy 934 GGAACGGGGCTGTTTATACCACTGAGGACGAGGAC-GTGAGCCCCCGCTCCACCTC 992
Db 781 GGAACGGG--CTCGTTATCACCAGTGAGGACGAGGCGGTGAGCCCCCGCTGAATCTCT 838
Qy 993 TGCTGTTTAAACACCCAGCCATCCCTTCTTTTCAAAAGGGATCCTTTTCATAGGAGAAACACA 1052
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Db 899 CTGGAGGAGATCTTGACAGCATTTGGTTGCGCG 932

RESULT 13
LOCUS      AL555978             1076 bp          mRNA          linear          EST 30-MAR-2004
DEFINITION AL555978 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DK010Y111 5-PRIME, mRNA sequence.
ACCESSION  AL555978
VERSION     AL555978.3  GI:45860699
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 1076)
AUTHORS     Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31277782.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2801.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DK010AE06QPl&c=2801.r.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK010Y111"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      52.2%; Score 845.8; DB 1; Length 1076;
Best Local Similarity 96.3%; Pred. No. 3.5e-177;

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Matches 891; Conservative 14; Mismatches 16; Indels 4; Gaps 4;			
QY	1	CGCCATGGCACTGACGGGATCTCGGTCATGGAGCTGTCGGCTGCGCCCGGCGCGTT	60
Db	73	CGCCATGGCACTGACGGGATCTCGGTCATGGAGCTGTCGGCTGCGCCCGGCGCGTT	132
QY	61	CTGTGCTATGGTCTCTGGCTGACTTTCGGGGGCGGTGTGTACGGGTGACCGCGCCCGGCTC	120
Db	133	CTGTGCTATGGTCTCTGGCTGACTTTCGGGGGCGGTGTGTACGGGTGACCGCGCCCGGCTC	132
QY	121	CCGCTACGACGTAGCGCGCTTGGCCCGGGGCAAGCGTCTGCTAGTGTGACCTGAAGCA	180
Db	193	CCGCTACGACGTAGCGCGCTTGGCCCGGGGCAAGCGTCTGCTAGTGTGACCTGAAGCA	252
QY	181	GCCGCGGGGAGCGCGCTGCTGCGGCTGTGTCAAGCGGTGCGATGCTGCTGGAGCC	240
Db	253	GCCGCGGGGAGCGCGCTGCTGCGGCTGTGTCAAGCGGTGCGATGCTGCTGGAGCC	312
QY	241	CTTCCGCGCGGTGTCTCATGGAGAACTCCAGCTGGGCGGACAGATTCTGACGGGAAAA	300
Db	313	CTTCCGCGCGGTGTCTCATGGAGAACTCCAGCTGGGCGGACAGATTCTGACGGGAAAA	372
QY	301	TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAGCTTTCGCCGTT	360
Db	373	TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAGCTTTCGCCGTT	432
QY	361	AGCTGGCCAGATATCAACTATTGCTTGTGCTGAGTGTCTCTCAAAATTCGCAAG	420
Db	433	AGCTGGCCAGATATCAACTATTGCTTGTGCTGAGTGTCTCTCAAAATTCGCAAG	492
QY	421	TGCTGAGAAATCCGTATGCGCCGCTGATCTCTCGGCTGACTTTGCTGGTGGCTTAT	480
Db	493	TGCTGAGAAATCCGTATGCGCCGCTGATCTCTCGGCTGACTTTGCTGGTGGCTTAT	552
QY	481	GTGTGCACTGGGAT-TATAATGGCTCTTTTTCACCGCACACGACATGCAAGGTCAGG	539
Db	553	GTGTGCACTGGGATATATAATGGCTCTTTTTCACCGCACACGACATGCAAGGTCAGG	612
QY	540	TCATTGATCAATATGCTGGAAGGACACGATATTTAGTTCTTTTCTGTGAAAACTC	599
Db	613	TCATTGATCAATATGCTGGAAGGACACGATATTTAGTTCTTTTCTGTGAAAACTC	672
QY	600	AGAAATCGAGTCTGTGGAGACCTCGAGGACAGAACATGTTGGATGGTGGAGACCTT	659
Db	673	AGAAATCGAGTCTGTGGAGACCTCGAGGACAGAACATGTTGGATGGTGGAGACCTT	732
QY	660	TCTATACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGTGAGCAATAGAACCC	719
Db	733	TCTATACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTGTGAGCAATAGAACCC	792
QY	720	AGTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTCCTCAATCAG	779
Db	793	AGTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTCCTCAATCAG	852
QY	780	TGAGCATGGATGATGGCCAGAAATGAAGAAAGTTTTCAGATGATTTTGAAGAAGA	839
Db	853	TGAGCATGGATGATGGCCAGAAATGAAGAAAGTTTTCAGATGATTTTGAAGAAGA	912
QY	840	CGAAGCAGAGTGGTGTCAAAATCTTTGACGGCAGATGCTGTGTGACTCCGGTTCTGA	899
Db	913	SGAA-GSAGAGTGGTGKAAATCTTTGACGG-ACAGATG-CTGTGTGRMTCGGTTCTGM	969
QY	900	CTTTTGAGGAGGTGTTTCATCAAGA	924
Db	970	TTTTTGAGGAGGTGTTTCATCAATAA	994

RESULT 14  
AL551698  
LOCUS  
DEFINITION  
AL551698 Homo sapiens PLACENTA COT 25-NORMALIZED  
clone CS0D1062YP05 5-PRIME, mRNA sequence.  
AL551698

VERSION KEYWORDS SOURCE ORGANISM			
AL551698.3	GI:45856497	Homo sapiens (human)	
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 990)			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
On Feb 15, 2001 this sequence version replaced gi:31273514.			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2801.r			
For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0D1062CH03QPl&c=2801.r.			
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Query Match 50.7%; Score 822.2; DB 1; Length 990;			
Best Local Similarity 95.1%; Pred. No. 6.1e-172;			
Matches 855; Conservative 11; Mismatches 31; Indels 2; Gaps 2;			
QY	1	CGCCATGGCACTGACGGGATCTCGGTCATGGAGCTGTCGGCTGCGCCCGGCGCGTT	60
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QY	61	CTGTGCTATGGTCTCTGGCTGACTTTCGGGGGCGGTGTGTACGGGTGACCGCGCCCGGCTC	120
Db	73	CTGTGCTATGGTCTCTGGCTGACTTTCGGGGGCGGTGTGTACGGGTGACCGCGCCCGGCTC	132
QY	121	CCGCTACGACGTAGCGCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTGAGCTGAAGCA	180
Db	133	CCGCTACGACGTAGCGCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTGAGCTGAAGCA	192
QY	181	GCCGCGGGGAGCGCGCTGCTGCGGCTGTGTCAAGCGGTGCGATGCTGCTGGAGCC	240
Db	193	GCCGCGGGGAGCGCGCTGCTGCGGCTGTGTCAAGCGGTGCGATGCTGCTGGAGCC	252
QY	241	CTTCCGCGCGGTGTCTCATGGAGAACTCCAGCTGGGCGGACAGATTCTGACGGGAAAA	300
Db	253	CTTCCGCGCGGTGTCTCATGGAGAACTCCAGCTGGGCGGACAGATTCTGACGGGAAAA	312
QY	301	TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAGCTTTCGCCGTT	360
Db	313	TCCAAGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAGCTTTCGCCGTT	372
QY	361	AGCTGGCCAGATATCAACTATTGCTTGTGCTGAGTGTCTCTCAAAATTCGCAAGAAG	420
Db	373	AGCTGGCCAGATATCAACTATTGCTTGTGCTGAGTGTCTCTCAAAATTCGCAAGAAG	432
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Db 553 CATTNATGCAAAATATGTTGGGAAGAACAGCATATTAAAGTTCTTTTCTGTGGAAAACTCA 612
Qy 601 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAACATGTTGGATGTTGGAGCACCTTT 660
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Qy 661 CTATACGACTTACAGGACAGCAGATCGGGGAATTCATGGCTGTTGGCAATAGAACCCCA 720
Db 673 CTATACGACTTACAGGACAGCAGATCGGGGAATTCATGGCTGTTGGCAATAGAACCCCA 732
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Qy 841 GAAGGACAGTGGTGTCAAAATCTTTTCAGCGCACAGATCCCTGTGTGATCTCGGTTCTGA 899
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BM723657
LOCUS
DEFINITION
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  UI-E-EJ0-aig-n-09-0-UI 5', mRNA sequence.
ACCESSION
  BM723657
VERSION
  BM723657.1 GI:19044988
KEYWORDS
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SOURCE
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  Organism
    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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  1 (bases 1 to 823)
REFERENCE
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
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  Genome Res. 6 (9), 791-806 (1996)
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
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  Seq primer: M13 Reverse.
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Best Local Similarity 99.1%; Pred. No. 4.9e-170;
Matches 816; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 61 TTCTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCC 120
Qy 719 CAGTTCTACAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATTCCTCCCAATCAG 778
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Qy 779 ATGAGCATGATGATTCGCCAGAAATGAAGAAGTTCAGCATGTTATTTGCAAAAGAAC 838
Db 181 ATGAGCATGATGATTCGCCAGAAATGAAGAAGTTCAGCATGTTATTTGCAAGAAC 240
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Db 301 ACTTTTTCAGGAGTGTTCATCATGATCAACAGGAAACGGGCTGTTTATCACCAGT 360
Qy 959 GAGGACGAGGACGTCAGCCCGCCCTGCTGCTGTTAAACACCCAGGACCATCCCT 1018
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Db 421 TCTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGA 480
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/clone_lib="UI-E-EJ0"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
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UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATTCAGAA; lens, CGATTAGGGA; eye anterior segment,
AATGCCGCTAT; optic nerve, CCAATTAAGTG; retina, CCGCC; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
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JOURNAL	Patent: US 6512094-A 107 28-JAN-2003;
	Corixa Corporation; Seattle, WA
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QY	481 GTGTGACCTGGGCACTTAAATGGCTCTTTTGGACCGCACACGCACTGACAAGGGTCAGGT 540
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DEFINITION	Sequence 107 from patent US 6329505.
ACCESSION	AR366923
VERSION	AR366923.1 GI:34599898
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 1621)
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J., Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and Day,C.H.
TITLE	Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL	Patent: US 6329505-A 107 11-DEC-2001;
FEATURES	Corixa Corporation; Seattle, WA
	Location/Qualifiers
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	source

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Db	1	CGCCATGCGACTGCGAGGCGATCTCGGTCAATGGAGCTGTCCGGCTCGGCCCGCGGCTT	60
Qy	61	CTGTGCTATGTCCTGGCTGATCTTGGGGCGCGTGTGTACGCTGGACCGGCGGCTC	120
Db	61	CTGTGCTATGTCCTGGCTGATCTTGGGGCGCGTGTGTACGCTGGACCGGCGGCTC	120
Qy	121	CCGCTACGACGTGAGCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA	180
Db	121	CCGCTACGACGTGAGCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGAACCTGAAGCA	180
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Qy	301	TCCAAGGCTTATATGCGCAGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCCGTT	360
Db	301	TCCAAGGCTTATATGCGCAGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCCGTT	360
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Db	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTCGCAAG	420
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Db	1081																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				</
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ACCESSION AR399959
VERSION AR399959.1 GI:40142893
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AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
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JOURNAL Patent: US 6620922-A 107 16-SEP-2003;
Corixa Corporation; Seattle, WA
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DEFINITION Sequence 107 from patent US 6630305.
ACCESSION AR405226
VERSION AR405226.1 GI:40154063
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 107 OCT-2003;
Corixa Corporation; Seattle, WA;
WOX;
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VERSION AR439430.1 GI:42665339
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6664377-A 107 16-DEC-2003; Corixa Corporation, Seattle, WA;
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VERSION AR563606.1 GI:53978657  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1621)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6759515-A 107 06-JUL-2004;  
Corixa Corporation; Seattle, WA  
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DEFINITION Sequence 107 from patent US 6800746.  
ACCESSION AR588592  
VERSION AR588592.1 GI:56635489  
KEYWORDS  
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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1621)  
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T. and Henderson, R. A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6800746-A 107 05-OCT-2004;  
Corixa Corporation; Seattle, WA  
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VERSION AR605412.1 GI:56657076  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1621)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedwick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6818751-A 107 16-NOV-2004;  
Corixa Corporation; Seattle, WA  
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ACCESSION AR653026  
VERSION AR653026.1 GI:67583271  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1621)  
AUTHORS Xu, J. and Dillon, D.C.  
TITLE Compounds for immunodiagnosis of prostate cancer and methods for their use  
JOURNAL Patent: US 6887660-A 107 03-MAY-2005;  
Corixa Corporation; Seattle, WA  
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VERSION AR656751.1 GI:67589829  
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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1621)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Panger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedwick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6894146-A 107 17-MAY-2005;  
Corixa Corporation; Seattle, WA  
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Result No.	Score	Query Match	Length	ID	Description
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2	1621	100.0	1621	3	US-09-030-607-107 Sequence 107, App
3	1621	100.0	1621	3	US-09-439-313-107 Sequence 107, App
4	1621	100.0	1621	3	US-09-352-616A-107 Sequence 107, App
5	1621	100.0	1621	3	US-09-232-149A-107 Sequence 107, App
6	1621	100.0	1621	3	US-09-159-812-107 Sequence 107, App
7	1621	100.0	1621	3	US-09-636-215-107 Sequence 107, App
8	1621	100.0	1621	3	US-09-685-166A-107 Sequence 107, App
9	1621	100.0	1621	3	US-09-115-453-107 Sequence 107, App
10	1621	100.0	1621	3	US-09-688-489-107 Sequence 107, App
11	1621	100.0	1621	3	US-09-679-426-107 Sequence 107, App
12	1621	100.0	1621	3	US-09-759-143-107 Sequence 107, App
13	1621	100.0	1621	3	US-09-651-236-107 Sequence 107, App
14	1621	100.0	1621	3	US-09-030-606-107 Sequence 107, App
15	1621	100.0	1621	3	US-09-657-279-107 Sequence 107, App
16	1621	100.0	1621	3	US-10-012-896-107 Sequence 107, App
17	1621	100.0	1621	5	US-09-116-134-107 Sequence 107, App
18	1621	100.0	1621	5	US-10-144-678A-107 Sequence 107, App
19	515	31.8	537	3	US-09-020-956-74 Sequence 74, Appl
20	515	31.8	537	3	US-09-030-607-74 Sequence 74, Appl
21	515	31.8	537	3	US-09-439-313-74 Sequence 74, Appl
22	515	31.8	537	3	US-09-352-616A-74 Sequence 74, Appl
23	515	31.8	537	3	US-09-232-149A-74 Sequence 74, Appl

24	515	31.8	537	3	US-09-159-812-74	Sequence 74, Appl
25	515	31.8	537	3	US-09-636-215-74	Sequence 74, Appl
26	515	31.8	537	3	US-09-685-166A-74	Sequence 74, Appl
27	515	31.8	537	3	US-09-115-453-74	Sequence 74, Appl
28	515	31.8	537	3	US-09-688-489-74	Sequence 74, Appl
29	515	31.8	537	3	US-09-679-426-74	Sequence 74, Appl
30	515	31.8	537	3	US-09-759-143-74	Sequence 74, Appl
31	515	31.8	537	3	US-09-651-236-74	Sequence 74, Appl
32	515	31.8	537	3	US-09-030-606-74	Sequence 74, Appl
33	515	31.8	537	3	US-09-657-279-74	Sequence 74, Appl
34	515	31.8	537	3	US-10-012-896-74	Sequence 74, Appl
35	515	31.8	537	5	US-09-116-134-74	Sequence 74, Appl
36	515	31.8	537	5	US-10-144-678A-74	Sequence 74, Appl
37	426.8	26.3	430	3	US-09-702-705-1504	Sequence 1504, Ap
38	426.8	26.3	430	3	US-09-736-457-1504	Sequence 1504, Ap
39	426.8	26.3	430	3	US-09-614-124B-1504	Sequence 1504, Ap
40	426.8	26.3	430	3	US-09-671-325-1504	Sequence 1504, Ap
41	426.8	26.3	430	3	US-09-658-824-1504	Sequence 1504, Ap
42	426.8	26.3	430	3	US-10-017-754-1504	Sequence 1504, Ap
43	426.8	26.3	430	3	US-09-651-563-1504	Sequence 1504, Ap
C 44	406.6	25.1	773	3	US-09-020-956-3	Sequence 3, Appli
C 45	406.6	25.1	773	3	US-09-030-607-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-020-956-107  
; Sequence 107, Application US/09020956  
; Patent No. 6261562  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillin, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/020,956  
; FILING DATE: 09-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 107:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1621 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-09-020-956-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGACACTCGAGGCGATCTCGGTCAATGAGCTGTCCGGCTTGGCCCCCGGGCCCGTT 60  
Db 1 CGCCATGACACTCGAGGCGATCTCGGTCAATGAGCTGTCCGGCTTGGCCCCCGGGCCCGTT 60  
QY 61 CTGTGCTATGTCCTGTGGCTGACTTCGGGGCGGTGTGTGTAGCGTGGACCGGCCCGGCTC 120  
Db 61 CTGTGCTATGTCCTGTGGCTGACTTCGGGGCGGTGTGTGTAGCGTGGACCGGCCCGGCTC 120  
QY 121 CCGCTACGACGTGAGCCGCTTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGGAAGCA 180  
Db 121 CCGCTACGACGTGAGCCGCTTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGGAAGCA 180  
QY 181 GCGGGGGAGCGCGCTGTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGTGGAGCC 240  
Db 181 GCGGGGGAGCGCGCTGTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGTGGAGCC 240  
QY 241 CTTCCGCGCGGTGTGATGGAGAACTCCAGCTGGGCGCAGAGATTCGACAGCGGAAAA 300  
Db 241 CTTCCGCGCGGTGTGATGGAGAACTCCAGCTGGGCGCAGAGATTCGACAGCGGAAAA 300  
QY 301 TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360  
Db 301 TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360  
QY 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAAATGGCAGAG 420  
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAAATGGCAGAG 420  
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Db 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGAT 780  
QY 781 GAGCATGATGATTTGGCCAGAAATCAAGAAGTTTCAGATGATTTTGAAGAAGAC 840  
Db 781 GAGCATGATGATTTGGCCAGAAATCAAGAAGTTTCAGATGATTTTGAAGAAGAC 840  
QY 841 GAAAGCAGATGGTGTCAAACTTTTGGCGGACAGATGCTGTGTGACTCCGGTTCTGAC 900  
Db 841 GAAAGCAGATGGTGTCAAACTTTTGGCGGACAGATGCTGTGTGACTCCGGTTCTGAC 900  
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Db 901 TTTTGAAGAGGTGTTTTCATCATGATCAAAAGGACCGGGCTCGTTTATCACCAGTGA 960  
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Db 961 GGAGCAGAGCTGAGCCCGCCCTGACCTGCTGTTTAAACCCCGAGCCATCCCTTC 1020  
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Db 1021 TTTTAAAAAGGGATCTTTTATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT 1080

QY 1081 CAGCCGGAAGAGATTATTCAGCTTAACCTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140  
Db 1081 CAGCCGGAAGAGATTATTCAGCTTAACCTCAGATAAAATCATTTGAAAGTAAATAGGTAAA 1140  
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Db 1141 AGCTAGTCTCTAACTTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200  
QY 1201 TAGAGTAACATTAACATTTGATGATGGAACATGAGGAAACATGAGGAAACAGTATTTACAGTGTCTTA 1260  
Db 1201 TAGAGTAACATTAACATTTGATGATGGAACATGAGGAAACATGAGGAAACAGTATTTACAGTGTCTTA 1260  
QY 1261 CCAGTCTAAATCAAGAAAGAAATACAGACTCTGATTTCTACAGTCAATGATTAATTTCTAAA 1320  
Db 1261 CCAGTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTCAATGATTAATTTCTAAA 1320  
QY 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAACTTTTGGGTACTTATACATAATATGGT 1380  
Db 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAACTTTTGGGTACTTATACATAATATGGT 1380  
QY 1381 AGTTATTTCTGCTTCCAGTTTGGTGTGATATTTTGTGATATTAAGATTTCTTGACTTATA 1440  
Db 1381 AGTTATTTCTGCTTCCAGTTTGGTGTGATATTTTGTGATATTAAGATTTCTTGACTTATA 1440  
QY 1441 TTTTGAATGGTCTTAGTGAAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500  
Db 1441 TTTTGAATGGTCTTAGTGAAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500  
QY 1501 ATTTACACTCTTGATTTCAATGTTAGAAAATGAGAAAATGCCACAAATTTGATGGTGAT 1560  
Db 1501 ATTTACACTCTTGATTTCAATGTTAGAAAATGAGAAAATGCCACAAATTTGATGGTGAT 1560  
QY 1561 AAAAGTCAGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620  
Db 1561 AAAAGTCAGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620  
QY 1621 A 1621  
Db 1621 A 1621

## RESULT 2

US-09-030-607-107  
; Sequence 107, Application US/09030607  
; Patent No. 6262245  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,607  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.427C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 107:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1621 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; US-09-030-607-107

Query Match

Best Local Similarity 100.0%; Score 1621; DB 3; Length 1621;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGCCATGGCACTGCAGGCGATCTCGGTCAATGAGCTGTCCGGCTGGCCCGGCCCGCTT 60
DB 1 CGCCATGGCACTGCAGGCGATCTCGGTCAATGAGCTGTCCGGCTGGCCCGGCCCGCTT 60
QY 61 CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGGTGTGTACGCTGGACCGGCCGGCTC 120
DB 61 CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGGTGTGTACGCTGGACCGGCCGGCTC 120
QY 121 CGCTACGACGTGAGCGCTTGGCCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCA 180
DB 121 CGCTACGACGTGAGCGCTTGGCCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCA 180
QY 181 GCGCGGGAGCGCGCGTCTGGGGCGGTCTGTGCAAGCGGTGGATGTCTGTGGAGCC 240
DB 181 GCGCGGGAGCGCGCGTCTGGGGCGGTCTGTGCAAGCGGTGGATGTCTGTGGAGCC 240
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DB 241 CTTTCGCGCGGTGTCTATGAGAACTCCAGCTGGGCCAGAGATTCGACGGGAAAA 300
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DB 361 AGCTGGCCAGATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAG 420
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DB 421 TGGTGAATCCGTATGATCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTAT 480
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QY 541 CATTTAGTCAATATGGTGGAGGAAACAGCATATTTAAGTCTTTTCTGTGAAAACCTCA 600
DB 541 CATTTAGTCAATATGGTGGAGGAAACAGCATATTTAAGTCTTTTCTGTGAAAACCTCA 600
QY 601 GAAATCGACTGTGGAGACCTTCGAGCAGACATGTTGGATGGTGGACCTTTT 660
DB 601 GAAATCGACTGTGGAGACCTTCGAGCAGACATGTTGGATGGTGGAGACCTTTT 660
QY 661 CTATACGACTTACAGCAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGACCCCA 720
DB 661 CTATACGACTTACAGCAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGACCCCA 720
QY 721 GTTCTACGAGCTGCTGATCAAGGACTTCGACTAAAGTCTGATGAATTTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGCTGATCAAGGACTTCGACTAAAGTCTGATGAATTTCCCAATCAGAT 780
QY 781 GAGCATGGATGATGGCCAGAAATGAGAGAGTTTGCAGATGATTTTGCAGAGAC 840
DB 781 GAGCATGGATGATGGCCAGAAATGAGAGAGTTTGCAGATGATTTTGCAGAGAC 840
QY 841 GAAGGCAGAGTGGTCAAACTTTTGAACGCGCAGATGCTGTGTGACTCCGGTCTGAC 900
DB 841 GAAGGCAGAGTGGTCAAACTTTTGAACGCGCAGATGCTGTGTGACTCCGGTCTGAC 900
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## RESULT 3

US-09-439-313-107

; Sequence 107, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqi

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER



; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-352-616A-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGCCTAGGAGCTGAGCGGCTCTCGGTCTGATGAGCTGTCGGGCTGCGCCCGGCGCGTT 60
DB 1 CGCCTAGGAGCTGAGCGGCTCTCGGTCTGATGAGCTGTCGGGCTGCGCCCGGCGCGTT 60

QY 61 CTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 121 CCCTAGGAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 CCCTAGGAGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

QY 181 GCGCGGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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QY 241 CTTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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QY 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGGCTTCTGCCGGTT 360
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QY 361 AGCTGCCAGGATCAACTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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QY 421 TGGTGAGATCCGTATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 TGGTGAGATCCGTATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

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QY 541 CATTTGATGCAATATGCTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTTGGAAGAACTCA 600
DB 541 CATTTGATGCAATATGCTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTTGGAAGAACTCA 600

QY 601 GAAATCGAGTCTGTGGAGGACCTCGAGGACAGACATGTTGGATGCTGGAGCACTTT 660
DB 601 GAAATCGAGTCTGTGGAGGACCTCGAGGACAGACATGTTGGATGCTGGAGCACTTT 660

QY 661 CTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATGAACCCCA 720
DB 661 CTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATGAACCCCA 720

QY 721 GTTCTACGAGCTGCTGATCAAGGACTTGAATTAAGTCTGATGAATCTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGCTGATCAAGGACTTGAATTAAGTCTGATGAATCTCCCAATCAGAT 780

QY 781 GAGCATGGATGATTTGGCCAGAAATGAAGAGATTTGAGATGATTTTGCAGAGAGAC 840
DB 781 GAGCATGGATGATTTGGCCAGAAATGAAGAGATTTGAGATGATTTTGCAGAGAGAC 840

QY 841 GAAGGAGAGTGTGTCAATCTTTGACGCGCAGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 GAAGGAGAGTGTGTCAATCTTTGACGCGCAGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

QY 901 TTTTGAAGGAGTTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTATCACAGTGA 960
DB 901 TTTTGAAGGAGTTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTATCACAGTGA 960
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QY 961 GGAGCAGGAGCTGAGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 GGAGCAGGAGCTGAGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

QY 1021 TTTCAAAGGAGTCTTTTCATAGGAGAAACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
DB 1021 TTTCAAAGGAGTCTTTTCATAGGAGAAACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080

QY 1081 CAGCGCGAGGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATTAAGGTAAA 1140
DB 1081 CAGCGCGAGGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATTAAGGTAAA 1140

QY 1141 AGCTAGTCTCTAACTTCCAGGCGCCAGGCTCAAGTGAATTTGAATACTCATTTCAGTG 1200
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DB 1201 TAGAGTAACACATAACATTTGATGATGATAAATGGAACATGGAGGAAACAGTATTCAGTGCTCTTA 1260

QY 1261 CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320
DB 1261 CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320

QY 1321 AATGGTTATCATTAGGGCTTTTGAATTTATAAAACCTTTGGGTACTTATACATAATTTATGGT 1380
DB 1321 AATGGTTATCATTAGGGCTTTTGAATTTATAAAACCTTTGGGTACTTATACATAATTTATGGT 1380

QY 1381 AGTTATCTGCTTCCAGTTGCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
DB 1381 AGTTATCTGCTTCCAGTTGCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440

QY 1441 TTTTGAAGTGGTCTAGTGAAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500
DB 1441 TTTTGAAGTGGTCTAGTGAAAGAAAGATGATATTTCTTGAAGACATCGATATACATTT 1500

QY 1501 ATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAAATGCCACAAATTTGATGCTGAT 1560
DB 1501 ATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAAATGCCACAAATTTGATGCTGAT 1560

QY 1561 AAAAGTCAGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620
DB 1561 AAAAGTCAGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620

QY 1621 A 1621
DB 1621 A 1621
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## RESULT 5

US-09-232-149A-107

; Sequence 107, Application US/09232149A  
; Patent No. 6465611  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; FILE REFERENCE: 210121.427C6  
; CURRENT APPLICATION NUMBER: US/09/232,149A  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-232-149A-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







121 CCGTACGACGAGCGCTTGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCA 180  
121 CCGCTACGAGCGTGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCA 180  
181 GCGCGGGAGCGCGCTGCTCGGGGTCTGTGCAAGCGGTGCGATGTGCTCGAGCC 240  
181 GCGCGGGAGCGCGCTGCTCGGGGTCTGTGCAAGCGGTGCGATGTGCTCGAGCC 240  
241 CTTCCGCGCGGTGTGTCATGCGAAGAACTCCAGCTGGGCCGAGAGATTTGCGAGCGGAAA 300  
241 CTTCCGCGCGGTGTGTCATGCGAAGAACTCCAGCTGGGCCGAGAGATTTGCGAGCGGAAA 300  
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301 TCCAGGCTTATTTATGCGAGGCTGAGTGAATTTGCGCAGTCAGGAAGCTTCTGCGGGTT 360  
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361 AGCTGGCCAGATCAACTATTTGGCTTTGTGTCAGGTGTTCTCAAAAATTTGGCAGAAG 420  
421 TGGTCAGATCGATGCGTATGCGCGCTGAACTCTCTGCTGACTTTGCTGGTGGCTTAT 480  
421 TGGTCAGATCGATGCGTATGCGCGCTGAACTCTCTGCTGACTTTGCTGGTGGCTTAT 480  
481 GTGTGCACTGGGCATTTAATGGCTCTTTTTCACCGCCACACGCACTGCAAGGGTCAGGT 540  
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601 GAAATCGAGTCTGTGGAGGACCTCGAGGACAGACATGTTGGATGTTGGAGCACCTTT 660  
601 GAAATCGAGTCTGTGGAGGACCTCGAGGACAGACATGTTGGATGTTGGAGCACCTTT 660  
661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGCTGTGGAGCAATAGAACCCCA 720  
661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGCTGTGGAGCAATAGAACCCCA 720  
721 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780  
721 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780  
781 GAGCATGATGATTTGCCAGAAATGAAGAGAGTTTGCAGATGATTTTGCAGAAAGAC 840  
781 GAGCATGATGATTTGCCAGAAATGAAGAGAGTTTGCAGATGATTTTGCAGAAAGAC 840  
841 GAAGGACAGATGTTGTCAAATCTTTGACGCGACAGATGCTGTGACTCCGGTTCTGAC 900  
841 GAAGGACAGATGTTGTCAAATCTTTGACGCGACAGATGCTGTGACTCCGGTTCTGAC 900  
901 TTTTGGAGGAGTTGTTTCATCATGATCACAAGGAACGGGCTCGTTTATCACCAGTGA 960  
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961 GGAGCAGACGTTAGCGCCCGCCCTGCACTCTGCTTTAAACCCCGCCATCCCTTC 1020  
961 GGAGCAGACGTTAGCGCCCGCCCTGCACTCTGCTTTAAACCCCGCCATCCCTTC 1020  
1021 TTTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATT 1080  
1021 TTTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATT 1080  
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1141 AGCTAGTCTTAACCTCAGGCGCCAGCGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200  
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1201 TAGAGTAACACATAATTTGATGATGTAAGAACATGGAGAACAGTATTACAGTGTCTTA 1260

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1261 CCACCTTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320  
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1321 AATGTTATCATTAAGGCTTTTGTATTTATAAAACTTTTGGTACTTTATATAAATTTATGTT 1380  
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1621 A 1621  
1621 A 1621

RESULT 7

US-09-636-215-107  
; Sequence 107, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Panger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215  
; CURRENT FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 852  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-636-215-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGCCATGCACTGCGGGCATCTCGGTGATGAGTGTCCGGCTTGGCCCGGCGCTTT  
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Query Match		100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 1621; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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DB	1	CGCCATGGCACTGAGGGGCAATCTCGGTATGAGAGCTGTCCGGCTCGGCCCGGGCCCGGTT 60
QY	61	CTGTGCTATGGTCTTGGTGAATCTCGGGCGGTGTGACGCTGCGACCGGGCCCGGCTC 120
DB	61	CTGTGCTATGGTCTTGGTGAATCTCGGGCGGTGTGACGCTGCGACCGGGCCCGGCTC 120
QY	121	CCGCTACGAGCTGAGCGGCTTGGCCGGGCAAGCGCTCGTAGTCTGAGACTGAGCA 180
DB	121	CCGCTACGAGCTGAGCGGCTTGGCCGGGCAAGCGCTCGTAGTCTGAGACTGAGCA 180
QY	181	GCCGCGGGAGCCGCGTGTGCGGGCTGTGTCAGAGCGGTGCGATGTCGTGAGGC 240
DB	181	GCCGCGGGAGCCGCGTGTGCGGGCTGTGTCAGAGCGGTGCGATGTCGTGAGGC 240
QY	241	CTTCCGCGGGTGTGATGAGAGAACTCCAGCTGGGCCAGAGATCTCGAGCGGAAA 300
DB	241	CTTCCGCGGGTGTGATGAGAGAACTCCAGCTGGGCCAGAGATCTCGAGCGGAAA 300
QY	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAGCTTCTGCCGTT 360
DB	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAGCTTCTGCCGTT 360
QY	361	AGTGGCCAGATATCAACTATTTGGTGTGTCAGGTGTTCTCAAAAATTGGCAGAAG 420
DB	361	AGTGGCCAGATATCAACTATTTGGTGTGTCAGGTGTTCTCAAAAATTGGCAGAAG 420
QY	421	TGCTGAGATCCGATGATGCCCCGCTGAATCTCTGGGCTGACTTGTGGTGGCTTAT 480
DB	421	TGCTGAGATCCGATGATGCCCCGCTGAATCTCTGGGCTGACTTGTGGTGGCTTAT 480
QY	481	GTGTGCACTGGGCATTTAATGCTCTTTTGAACGACACACGACCTGACAAGGTCAGGT 540
DB	481	GTGTGCACTGGGCATTTAATGCTCTTTTGAACGACACACGACCTGACAAGGTCAGGT 540
QY	541	CATTGATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTCTGTGGAATACTCA 600
DB	541	CATTGATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTCTGTGGAATACTCA 600
QY	601	GAAATCGACTCTGCGGAGACCTCGAGACAGACATGTTGGATGGTGGACACCTTT 660
DB	601	GAAATCGACTCTGCGGAGACCTCGAGACAGACATGTTGGATGGTGGACACCTTT 660
QY	661	CTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
DB	661	CTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
QY	721	GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATCTTCCCAATCAGAT 780
DB	721	GTTCTACGAGCTGCTGATCAAGGACTTGGACTTAAAGTCTGATGAATCTTCCCAATCAGAT 780
QY	781	GAGCATGATGATGTCGACCAAAATGAAGAAGTTGACATGATTTGCAAGAAGAC 840
DB	781	GAGCATGATGATGTCGACCAAAATGAAGAAGTTGACATGATTTGCAAGAAGAC 840
QY	841	GAAAGCAGAGTGTGTCAAATCTTTGACGACAGATGCTGTGACTCCGGTCTGAC 900
DB	841	GAAAGCAGAGTGTGTCAAATCTTTGACGACAGATGCTGTGACTCCGGTCTGAC 900
QY	901	TTTTGAGGAGTGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTTATCACCAGTGA 960
DB	901	TTTTGAGGAGTGTGTTTCATCATGATCACAAAGGAAACGGGCTCGTTTTATCACCAGTGA 960
QY	961	GGAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTTAAACACCCAGCAATCCCTTC 1020
DB	961	GGAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTTAAACACCCAGCAATCCCTTC 1020
QY	1021	TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATATTTGAAGATTTGGATT 1080

DB	1021	TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTTGAAGATTTGGATT 1080
QY	1081	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAAATAGGTAAA 1140
DB	1081	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAAATAGGTAAA 1140
QY	1141	AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTCAGTG 1200
DB	1141	AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTCAGTG 1200
QY	1201	TAGAGTAACACATAACATTTGATGATGGAACATGAGGAGAACAGTATTACAGTGTCTTA 1260
DB	1201	TAGAGTAACACATAACATTTGATGATGGAACATGAGGAGAACAGTATTACAGTGTCTTA 1260
QY	1261	CCACTCTAATCAAGAAAGAAATTCAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
DB	1261	CCACTCTAATCAAGAAAGAAATTCAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320
QY	1321	AATGGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATCTATAAATATGTT 1380
DB	1321	AATGGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATCTATAAATATGTT 1380
QY	1381	AGTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
DB	1381	AGTATTCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
QY	1441	TTTTGAATGGGTTCTAGTGAAAGAAATGATATTTCTTGAAGACATGATATACATTT 1500
DB	1441	TTTTGAATGGGTTCTAGTGAAAGAAATGATATTTCTTGAAGACATGATATACATTT 1500
QY	1501	ATTTACACTCTTGTCTTACAAATGAGAAATGAGAAATGCCAAATTTGTTGTTGAT 1560
DB	1501	ATTTACACTCTTGTCTTACAAATGAGAAATGAGAAATGCCAAATTTGTTGTTGAT 1560
QY	1561	AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
DB	1561	AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620
QY	1621	A 1621
DB	1621	A 1621

RESULT 9

US-09-115-453-107

Sequence 107, Application US/09115453B

Patent No. 6657056

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

TITLE OF INVENTION: METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C4

CURRENT APPLICATION NUMBER: US/09/115,453B

CURRENT FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq For Windows Version 3.0

SEQ ID NO 107

LENGTH: 1621

TYPE: DNA

ORGANISM: Homo sapien

US-09-115-453-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGAGGGGCAATCTCGGTATGAGAGCTGTCCGGCTCGGCCCGGGCCCGGTT 60

DB 1 CGCCATGGCACTGAGGGGCAATCTCGGTATGAGAGCTGTCCGGCTCGGCCCGGGCCCGGTT 60

QY 61 CTGTGCTATGGTCTTCTGAGGAGCACTTCGGGCGCGTGTGTTACGCTGGACCGGCCCGGCTC 120

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Db 1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATCTACATGCAATTTACAGTG 1200
Qy 1201 TAGAGTAACACATAAATTTGTTATGTCATGGAACATGGAGGAAACAGTATTTACAGTGTCTTA 1260
Db 1201 TAGAGTAACACATAAATTTGTTATGTCATGGAACATGGAGGAAACAGTATTTACAGTGTCTTA 1260
Qy 1261 CCAGTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGTGATGATTTGAAATTTCTAAA 1320
Db 1261 CCAGTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGTGATGATTTGAAATTTCTAAA 1320
Qy 1321 AATGGTTATCAATAGGGCTTTTGAATTTATATAAACTTTGGGTACTTATATCTAAATATATGGT 1380
Db 1321 AATGGTTATCAATAGGGCTTTTGAATTTATATAAACTTTGGGTACTTATATCTAAATATATGGT 1380
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Db 1621 A 1621

RESULT 10
US-09-688-489-107
; Sequence 107, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-688-489-107
; Sequence 107, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-107
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181 GCGCGGGAGCGCGCGTCTGCGCGTCTGCAAGCGGTGCGATGCTGCTGAGCC 240  
241 CTTCCGCGCGGTGTCATGAGAACTCCAGCTGGCCGAGAGATTCACGCGGAAA 300  
241 CTTCCGCGCGGTGTCATGAGAACTCCAGCTGGCCGAGAGATTCACGCGGAAA 300  
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1081 CAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATAAGTAAA 1140  
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Db 1261 CCACTCTAATCAAGAAAGATTTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320  
Qy 1321 AATGTTTATCATTTAGGCTTTTGTATTTATAAACTTTGGGTACTTTATCTAAATTTATGTT 1380  
Db 1321 AATGTTTATCATTTAGGCTTTTGTATTTATAAACTTTGGGTACTTTATCTAAATTTATGTT 1380  
Qy 1381 AGTTATCTGCTTCCAGTTTCTGCTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440  
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Qy 1621 A 1621  
Db 1621 A 1621

RESULT 11  
US-09-679-426-107  
; Sequence 107, Application US/09679426  
; Patent No. 6759515  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C20  
; CURRENT APPLICATION NUMBER: US/09/679,426  
; CURRENT FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 895  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-679-426-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1621 A 1621
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## RESULT 12

US-09-759-143-107  
; Sequence 107, Application US/09759143  
; Patent No. 6800746

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Barrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-759-143-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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REFERENCE/DOCKET NUMBER: 210121.428C3  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 107:  
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LENGTH: 1621 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-030-606-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-657-279-107  
Sequence 107, Application US/09657279  
Patent No. 6894146  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Devin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.

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; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-107

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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SUMMARIES

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2	1621	100.0	1621	3	US-09-780-669-107
3	1621	100.0	1621	3	US-09-030-606-107
4	1621	100.0	1621	3	US-09-822-827-107
5	1621	100.0	1621	3	US-09-115-453-107
6	1621	100.0	1621	3	US-09-232-880-107
7	1621	100.0	1621	3	US-09-895-793-107
8	1621	100.0	1621	3	US-09-895-814-107
9	1621	100.0	1621	6	US-10-012-896-107
10	1621	100.0	1621	6	US-10-010-940-107
11	1621	100.0	1621	7	US-10-144-678A-107
12	1621	100.0	1621	8	US-10-294-025-107
13	1621	100.0	1621	8	US-10-688-838-107
14	1621	100.0	1621	16	US-11-234-786-107
15	1577.4	97.3	2376	9	US-10-357-930-21284
16	1577.4	97.3	2376	9	US-10-357-930-21872
17	1577.4	97.3	2376	9	US-10-357-930-25228

18	1577.4	97.3	2376	9	US-10-357-930-27126
19	1575.8	97.2	2069	6	US-10-205-823-25
20	1575.8	97.2	2069	13	US-11-051-454-25
21	1574.2	97.1	2005	3	US-09-967-305-1
22	1574.2	97.1	2005	3	US-09-967-305-10
23	1574.2	97.1	2005	7	US-10-210-120-104
24	1574.2	97.1	2005	10	US-10-909-035-104
25	1574.2	97.1	2069	3	US-09-967-305-4
26	1574.2	97.1	2069	6	US-10-205-823-17
27	1574.2	97.1	2069	13	US-11-051-454-17
28	1574.2	97.1	3184	16	US-11-203-526-3
29	1524.8	94.1	2068	7	US-10-295-027-1134
30	1524.8	94.1	2068	8	US-10-316-540-11
31	1524.8	94.1	2068	10	US-10-756-149-1746
32	1245.4	76.8	2946	6	US-10-205-823-29
33	1245.4	76.8	2946	8	US-10-316-540-13
34	1245.4	76.8	2946	13	US-11-051-454-29
35	1243.8	76.7	3023	3	US-09-967-305-8
36	1243.8	76.7	3023	6	US-10-205-823-21
37	1243.8	76.7	3023	13	US-11-051-454-21
38	1142.8	70.5	1146	3	US-09-967-305-3
39	1134.4	70.0	2626	6	US-10-205-823-27
40	1134.4	70.0	2626	13	US-11-051-454-27
41	1132.8	69.9	3654	3	US-09-967-305-6
42	1132.8	69.9	3654	6	US-10-205-823-19
43	1132.8	69.9	3654	13	US-11-051-454-19
44	1132.8	69.9	3654	16	US-11-203-526-5
45	940	58.0	1039	8	US-10-378-029-3

ALIGNMENTS

RESULT 1

US-09-759-143-107  
; Sequence 107, Application US/09759143  
; Patent No. US200202248A1

GENERAL INFORMATION:

- APPLICANT: Xu Jiangchun
- APPLICANT: Dillon, Davin C.
- APPLICANT: Mitchem, Jennifer L.
- APPLICANT: Harlocker, Susan L.
- APPLICANT: Jiang, Yuqui
- APPLICANT: Henderson, Robert A.
- APPLICANT: Kalos, Michael D.
- APPLICANT: Fanger, Gary R.
- APPLICANT: Retter, Marc W.
- APPLICANT: Stolk, John A.
- APPLICANT: Day, Craig H.
- APPLICANT: Vedvick, Thomas S.
- APPLICANT: Carter, Darrick
- APPLICANT: Li, Samuel
- APPLICANT: Wang, Aijun
- APPLICANT: Skeiky, Yasir A.W.
- APPLICANT: Hepler, William
- TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
- TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
- FILE REFERENCE: 210121.427C23
- CURRENT APPLICATION NUMBER: US/09/759,143
- CURRENT FILING DATE: 2001-01-12
- NUMBER OF SEQ ID NOS: 934
- SOFTWARE: FastSeq for Windows Version 3.0
- SEQ ID NO 107
- LENGTH: 1621
- TYPE: DNA
- ORGANISM: Homo sapien
- US-09-759-143-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCAGTGGGATCTCGGTGATGGAGTGTCGGGCTGGCCCGGCCGCTT 60

Db 1 CGCATGCACTCGAGGCACTCGGTATGAGAGCTGTCGGGCTCGGCCCCGGGCGGTT 60  
Qy 61 CTGTGCTATGTCCTGGCTGACTTCGCGGGCGGTGTGGTACGCGTGGACCGGCCCCGGCTC 120  
Db 61 CTGTGCTATGTCCTGGCTGACTTCGCGGGCGGTGTGGTACGCGTGGACCGGCCCCGGCTC 120  
Qy 121 CGGTACGAGTGAAGCCCTTGGGCGGGGCAAGGGCTCGGTAGTGTGGACCTGAAGCA 180  
Db 121 CGGTACGAGTGAAGCCCTTGGGCGGGGCAAGGGCTCGGTAGTGTGGACCTGAAGCA 180  
Qy 181 GCGCGGGGAGCGCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCC 240  
Db 181 GCGCGGGGAGCGCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCC 240  
Qy 241 CTTCCGCGCGGTGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCCTGACGGGGA 300  
Db 241 CTTCCGCGCGGTGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCCTGACGGGGA 300  
Qy 301 TCCAAGGCTTATTTATGTCAGGCTGAGTGGATTTGGGCCAGTCAGGAAGCTTCTGCCGGTT 360  
Db 301 TCCAAGGCTTATTTATGTCAGGCTGAGTGGATTTGGGCCAGTCAGGAAGCTTCTGCCGGTT 360  
Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGCAGAG 420  
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGCAGAG 420  
Qy 421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCTCGCTGACTTTGCTGGTGGTGGCTTTAT 480  
Db 421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCTCGCTGACTTTGCTGGTGGTGGCTTTAT 480  
Qy 481 GTGTGCACTGGGCATTTAATGGCTCTTTTGAACCGCACTGACGCACTGCAAGGGTCAGGT 540  
Db 481 GTGTGCACTGGGCATTTAATGGCTCTTTTGAACCGCACTGACGCACTGCAAGGGTCAGGT 540  
Qy 541 CATTGATCAATATGTTGGAGGAACAGCATATTTAAGTTCTTTCTGTGGAACCTCA 600  
Db 541 CATTGATCAATATGTTGGAGGAACAGCATATTTAAGTTCTTTCTGTGGAACCTCA 600  
Qy 601 GAAATCGAGTCTGTGGGAGCACCCTCGAGGACAGAACTATGTTGGATGGTGAGCACCTTT 660  
Db 601 GAAATCGAGTCTGTGGGAGCACCCTCGAGGACAGAACTATGTTGGATGGTGAGCACCTTT 660  
Qy 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720  
Db 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720  
Qy 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTAAGTCTGATGAATCTCCCAATCAGAT 780  
Db 721 GTTCTACGAGCTGTGATCAAGGACTTGGACTAAGTCTGATGAATCTCCCAATCAGAT 780  
Qy 781 GAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGCGATGTATTTGCAAGAAGAC 840  
Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGCGATGTATTTGCAAGAAGAC 840  
Qy 841 GAAGCAGAGTGGTCTCAAACTTTTGAACGCAAGATGCTGTGATCTCCGGTTCTGAC 900  
Db 841 GAAGCAGAGTGGTCTCAAACTTTTGAACGCAAGATGCTGTGATCTCCGGTTCTGAC 900  
Qy 901 TTTTGAAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACAGTGA 960  
Db 901 TTTTGAAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACAGTGA 960  
Qy 961 GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACCCCGAGCATCCCTTC 1020  
Db 961 GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACCCCGAGCATCCCTTC 1020  
Qy 1021 TTTTCAAAAGGGATCTTTTCATAGGAGAACACATGAGGAGATCTTGAAGAAATTTGGATT 1080  
Db 1021 TTTTCAAAAGGGATCTTTTCATAGGAGAACACATGAGGAGATCTTGAAGAAATTTGGATT 1080  
Qy 1081 CAGCGCCGAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAATAGGTAAA 1140

Db 1081 CAGCGCCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAAGGTAAA 1140  
Qy 1141 AGTAGTCTCTAACTTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCTATTTACAGTG 1200  
Db 1141 AGTAGTCTCTAACTTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCTATTTACAGTG 1200  
Qy 1201 TAGAGTAAACATAACTATGTCATGGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260  
Db 1201 TAGAGTAAACATAACTATGTCATGGAAACATGAGGAAACAGTATTACAGTGTCTTA 1260  
Qy 1261 CCACTCTAAATCAAGAAAGAAATTAAGACTCTGATCTACAGTGAATTTGAATTTCTAAA 1320  
Db 1261 CCACTCTAAATCAAGAAAGAAATTAAGACTCTGATCTACAGTGAATTTGAATTTCTAAA 1320  
Qy 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATTTATGGT 1380  
Db 1321 AATGGTTATCATTTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATTTATGGT 1380  
Qy 1381 AGTTATTTCTGCTTCCAGTTTCTTGATATATTTGTTGATATTAAAGATTCTTGACTTTATA 1440  
Db 1381 AGTTATTTCTGCTTCCAGTTTCTTGATATATTTGTTGATATTAAAGATTCTTGACTTTATA 1440  
Qy 1441 TTTTGAATGGGTTCTAGTGAAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500  
Db 1441 TTTTGAATGGGTTCTAGTGAAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500  
Qy 1501 ATTTACACTCTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTTGATATGGTGAT 1560  
Db 1501 ATTTACACTCTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTTGATATGGTGAT 1560  
Qy 1561 AAAAGTCACGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620  
Db 1561 AAAAGTCACGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620  
Qy 1621 A 1621  
Db 1621 A 1621

## RESULT 2

US-09-780-669-107  
; Sequence 107, Application US/09780669  
; Patent No. US2002005197A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; APPLICANT: Hurai, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C24  
; CURRENT APPLICATION NUMBER: US/09/780.669  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 943  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621

TYPE: DNA  
ORGANISM: Homo sapien  
US-09-780-669-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCATGGCACTGCGGGCATCTCGGTTCATGGAGCTGTCGGGCTGCGGCCCGCGCGCGGT 60  
DB 1 CGCATGGCACTGCGGGCATCTCGGTTCATGGAGCTGTCGGGCTGCGGCCCGCGCGCGGT 60  
QY 61 CTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 61 CTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
QY 121 CCCTAGCACTGAGCGCGCTGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGG 180  
DB 121 CCCTAGCACTGAGCGCGCTGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGG 180  
QY 181 GCCGCGGGAGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCT 240  
DB 181 GCCGCGGGAGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCT 240  
QY 241 CTTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 241 CTTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
QY 301 TCCAAGGCTTATTTATGCGAGGCTGAGTGAGTGGCGAGTGGCGAGTGGCGAGTGGCGAGT 360  
DB 301 TCCAAGGCTTATTTATGCGAGGCTGAGTGAGTGGCGAGTGGCGAGTGGCGAGTGGCGAGT 360  
QY 361 AGCTGCGCGAGTATCAACTATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB 361 AGCTGCGCGAGTATCAACTATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
QY 421 TGGTGAGATTCCTGATGCGCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 421 TGGTGAGATTCCTGATGCGCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
QY 481 GTGTGCACTGGGCACTTATATGCTCTTTTGGACCGGACACGCACTGCAAGGCTGAGGT 540  
DB 481 GTGTGCACTGGGCACTTATATGCTCTTTTGGACCGGACACGCACTGCAAGGCTGAGGT 540  
QY 541 CATTTGATGCAATATGCTGGAAGGACAGCATATTTAAAGTCTTTCTGTTGGAAGACTCA 600  
DB 541 CATTTGATGCAATATGCTGGAAGGACAGCATATTTAAAGTCTTTCTGTTGGAAGACTCA 600  
QY 601 GAAATCGAGTCTGTTGGAAGCACTCGAGGACAGACATGTTGGATGGTGGAGCACTTT 660  
DB 601 GAAATCGAGTCTGTTGGAAGCACTCGAGGACAGACATGTTGGATGGTGGAGCACTTT 660  
QY 661 CTATACGACTTACAGGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA 720  
DB 661 CTATACGACTTACAGGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA 720  
QY 721 GTTCTAGGAGTCTGATCAAGGACTTGGCACTTAAAGTCTGATGAACTTCCCAATCAGAT 780  
DB 721 GTTCTAGGAGTCTGATCAAGGACTTGGCACTTAAAGTCTGATGAACTTCCCAATCAGAT 780  
QY 781 GAGCATGATGATGCGGCAAGATGAAGAAGATTTGCAAGTATTTTCAAGAGAGAC 840  
DB 781 GAGCATGATGATGCGGCAAGATGAAGAAGATTTGCAAGTATTTTCAAGAGAGAC 840  
QY 841 GAAGGAGAGTGGTGTCAATCTTTGACGCGCACAGATGCTGTGCTCGGCTTCTGAC 900  
DB 841 GAAGGAGAGTGGTGTCAATCTTTGACGCGCACAGATGCTGTGCTCGGCTTCTGAC 900  
QY 901 TTTTGGAGGTTGTTTCATCATGATCAACACAGGAGCGGGCTGTTTATCACCAGTGA 960  
DB 901 TTTTGGAGGTTGTTTCATCATGATCAACACAGGAGCGGGCTGTTTATCACCAGTGA 960  
QY 961 GGAGGAGGAGTGGAGCGCGGCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

RESULT 3

US-09-030-606-107  
; Sequence 107, Application US/09030606  
; Patent No. US20020081580A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS  
; NUMBER OF SEQUENCES: 224  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,606  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-107

Query Match      100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CGCATGGCACTGCAGGCACTCTGGTCAATGGAGCTGTCGGGCTTGGCCCGCCGCGCCGTT  60
Db      1  CGCCATGGCACTGCAGGCACTCTGGTCAATGGAGCTGTCGGGCTTGGCCCGCCGCGGTT  60

Qy      61  CTGTGCTATGTCCTGGCTGACTTTCGGGGCGGTGTGGTACCGGTGGACCGGCGCGCTC  120
Db      61  CTGTGCTATGTCCTGGCTGACTTTCGGGGCGGTGTGGTACCGGTGGACCGGCGCGCTC  120

Qy      121  CCGTACGACGTAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA  180
Db      121  CCGTACGACGTAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA  180

Qy      181  CGCGGGGAGCGCGCTGCTGGCGCTCTGCAAGCGCTCGGATGCTGCTGGAGCC  240
Db      181  CGCGGGGAGCGCGCTGCTGGCGCTCTGCAAGCGCTCGGATGCTGCTGGAGCC  240

Qy      241  CTTCCGCGCGGTGTCTGAGGAACTCCAGCTGGGCGCCAGAGATTCTGCAGCGGAAA  300
Db      241  CTTCCGCGCGGTGTCTGAGGAACTCCAGCTGGGCGCCAGAGATTCTGCAGCGGAAA  300

Qy      301  TCCAAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAACTCTGCCGTT  360
Db      301  TCCAAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGAACTCTGCCGTT  360

Qy      361  AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAG  420
Db      361  AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTTGGCAG  420

Qy      421  TGGTGAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTTAT  480
Db      421  TGGTGAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTTAT  480

Qy      481  GTGTGCACTGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGACAGGCTCAGGT  540
Db      481  GTGTGCACTGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGACAGGCTCAGGT  540

Qy      541  CATTGATCAAAATATGGTGGAGGAAACAGCATATTTAAAGTCTTTCTGTGGAAACTCA  600
Db      541  CATTGATCAAAATATGGTGGAGGAAACAGCATATTTAAAGTCTTTCTGTGGAAACTCA  600

Qy      601  GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGAACTATTTGGATGGTGAGCACTTT  660
Db      601  GAAATCGAGTCTGTGGGAGCACTTCGAGGACAGAACTATTTGGATGGTGAGCACTTT  660

Qy      661  CTATACGACTTACAGACAGCAGATGGGGAATTCATGCGCTGTGGCAATAGAACCCCA  720
Db      661  CTATACGACTTACAGACAGCAGATGGGGAATTCATGCGCTGTGGCAATAGAACCCCA  720

Qy      721  GTTCTACGAGCTGCTGATCAAAAGGAACTTGGACTAAAGTCTGATGAACCTTCCCAAT  780
Db      721  GTTCTACGAGCTGCTGATCAAAAGGAACTTGGACTAAAGTCTGATGAACCTTCCCAAT  780
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## RESULT 4

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US-09-822-827-107
; Sequence 107, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
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Qy      781  GAGCATGGATGATTGGCCAGAAATGAGAAAGAGTTTGCAGATGCTATTTCAGAAAGAAC  840
Db      781  GAGCATGGATGATTGGCCAGAAATGAGAAAGAGTTTGCAGATGCTATTTCAGAAAGAAC  840

Qy      841  GAAGGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCGCTGTGCTGACTCCGGTCTG  900
Db      841  GAAGGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCGCTGTGCTGACTCCGGTCTG  900

Qy      901  TTTTGAGGAGTGTTCATCATGATCAAAACAAGGAAACGGGGCTCGTTTATCACCAGTGA  960
Db      901  TTTTGAGGAGTGTTCATCATGATCAAAACAAGGAAACGGGGCTCGTTTATCACCAGTGA  960

Qy      961  GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACACCCAGCCATCCCTTC  1020
Db      961  GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACACCCAGCCATCCCTTC  1020

Qy      1021  TTTCAAAAGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTCAAGAAATTTGGATT  1080
Db      1021  TTTCAAAAGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTCAAGAAATTTGGATT  1080

Qy      1081  CAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA  1140
Db      1081  CAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA  1140

Qy      1141  AGCTAGTCTCTAACTTCCAGGCCCGCCGCTCAAGTGAATTTGATCTGCAATTTACAGTG  1200
Db      1141  AGCTAGTCTCTAACTTCCAGGCCCGCCGCTCAAGTGAATTTGATCTGCAATTTACAGTG  1200

Qy      1201  TAGAGTAAACATAACTTGTATGTCATGGAACATGAGGAAACAGATTTACAGTGTCTTA  1260
Db      1201  TAGAGTAAACATAACTTGTATGTCATGGAACATGAGGAAACAGATTTACAGTGTCTTA  1260

Qy      1261  CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTCTACAGTGAATGAATTTCTAAA  1320
Db      1261  CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTCTACAGTGAATGAATTTCTAAA  1320

Qy      1321  AATGGTTATCATTTAGGCTTTTGAATTTTAAACTTTGGGTACTTACTATAATTTATGGT  1380
Db      1321  AATGGTTATCATTTAGGCTTTTGAATTTTAAACTTTGGGTACTTACTATAATTTATGGT  1380

Qy      1381  AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTTAAGATTTCTGACTTATA  1440
Db      1381  AGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATTTAAGATTTCTGACTTATA  1440

Qy      1441  TTTTGAATGGGTTCTAGTGAAAGAAAGGAATGATATATTTCTTGAAGACATCGATATTA  1500
Db      1441  TTTTGAATGGGTTCTAGTGAAAGAAAGGAATGATATATTTCTTGAAGACATCGATATTA  1500

Qy      1501  ATTTACACTCTTGAATTTCTACAAATGAGAAATGCGCAAAATTTGTATGTTGAT  1560
Db      1501  ATTTACACTCTTGAATTTCTACAAATGAGAAATGCGCAAAATTTGTATGTTGAT  1560

Qy      1561  AAAAGTCAGGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA  1620
Db      1561  AAAAGTCAGGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA  1620

Qy      1621  A 1621
Db      1621  A 1621
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; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-822-827-107

Query Match      100.0%; Score 1621; DB 3; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCATGGCACTGAGGAGCATCTCGGTATGAGAGCTGTCCGGCTGCGCCCGGCGCGTT 60
DB 1 CGCATGGCACTGAGGAGCATCTCGGTATGAGAGCTGTCCGGCTGCGCCCGGCGCGTT 60

QY 61 CTGTGCTATGGTCTGTGCTGACTTCCGGGCGCGTGTGGTACGGTGGACCGGCGCGCTC 120
DB 61 CTGTGCTATGGTCTGTGCTGACTTCCGGGCGCGTGTGGTACGGTGGACCGGCGCGCTC 120

QY 121 CCGCTACGAGCTGAGCGCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGAGCTGAAGCA 180
DB 121 CCGCTACGAGCTGAGCGCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGAGCTGAAGCA 180

QY 181 GCCGCGGGAGCGCGCTGCTGCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240
DB 181 GCCGCGGGAGCGCGCTGCTGCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240

QY 241 CTTCCGCGCGGTGTGATGAGAGAACTCCAGCTGGGCGCCAGAGATTCGAGCGGGAAAA 300
DB 241 CTTCCGCGCGGTGTGATGAGAGAACTCCAGCTGGGCGCCAGAGATTCGAGCGGGAAAA 300

QY 301 TCCAAGGCTATTATGTCAGGCTGAGTGATTTGGCCAGTCAAGAGCTTCTGCCGGETT 360
DB 301 TCCAAGGCTATTATGTCAGGCTGAGTGATTTGGCCAGTCAAGAGCTTCTGCCGGETT 360

QY 361 AGCTGGCCAGCATATCAACTATTGCTTGTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 420
DB 361 AGCTGGCCAGCATATCAACTATTGCTTGTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 420

QY 421 TGGTGAAGATCCGTATGCCCGCGTGAATCTCCCTGGCTGACTTTGCTGGTGGTGGCTTAT 480
DB 421 TGGTGAAGATCCGTATGCCCGCGTGAATCTCCCTGGCTGACTTTGCTGGTGGTGGCTTAT 480

QY 481 GTCTGCACTGGGCATTATATGCTCTTTTGGCCGACACGCTGACAGAGGCTCAGGT 540
DB 481 GTCTGCACTGGGCATTATATGCTCTTTTGGCCGACACGCTGACAGAGGCTCAGGT 540

QY 541 CATTTGATGCAATATGTTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGAATACTCA 600
DB 541 CATTTGATGCAATATGTTGGAAGGAAACAGCATATTTAAAGTTCTTTCTGTGGAATACTCA 600

QY 601 GAAATCAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTT 660
DB 601 GAAATCAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTT 660

QY 661 CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
DB 661 CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720

QY 721 GTTCTACGAGCTGCTGATCAAGAGCTTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT 780
DB 721 GTTCTACGAGCTGCTGATCAAGAGCTTTGGACTTAAAGTCTGATGAATCTCCCAATCAGAT 780

QY 781 GAGCATGGATGATTGGCCAGAAATGAAGAAGATTTGCAAGATGTTTTCGAAAGAGAC 840
DB 781 GAGCATGGATGATTGGCCAGAAATGAAGAAGATTTGCAAGATGTTTTCGAAAGAGAC 840

QY 841 GAAGGCGAGTGTGTCAATCTTTGACGCGACAGATGCTGTGACTCCGCTTCTGAC 900
DB 841 GAAGGCGAGTGTGTCAATCTTTGACGCGACAGATGCTGTGACTCCGCTTCTGAC 900

QY 901 TTTTGAGGAGTTGTTTCATCATGATCACAAGGAAACGGGGCTCGCTTTTATCACCAGTGA 960
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DB 901 TTTTGAGGAGTTGTTTCATCATGATCACAAGGAAACGGGGCTCGCTTTTATCACCAGTGA 960
QY 961 GGAGCAGGAGCTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGGCACTCCCTTC 1020
DB 961 GGAGCAGGAGCTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGGCACTCCCTTC 1020
QY 1021 TTTTAAAGGAGTCTTTTCATAGGAGAACACACTGAGGAGATATCTTTGAAGAATTTGGATT 1080
DB 1021 TTTTAAAGGAGTCTTTTCATAGGAGAACACACTGAGGAGATATCTTTGAAGAATTTGGATT 1080
QY 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAAATGAAGTAAA 1140
DB 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAAATGAAGTAAA 1140
QY 1141 AGCTAGTCTTAACCTTCCAGGCGCCCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1200
DB 1141 AGCTAGTCTTAACCTTCCAGGCGCCCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1200
QY 1201 TAGAGTAAACATACATTTGATGATGAAACATGAGGAGAACAGTATTTACAGTGTCTTA 1260
DB 1201 TAGAGTAAACATACATTTGATGATGAAACATGAGGAGAACAGTATTTACAGTGTCTTA 1260
QY 1261 CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1320
DB 1261 CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA 1320
QY 1321 AATGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGTACTTATCTAAATTTATGTT 1380
DB 1321 AATGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGTACTTATCTAAATTTATGTT 1380
QY 1381 AGTTATTTCTGCTTCCAGTTTCTGATATTTTGTGATATTTAGATTTCTTGACTTATA 1440
DB 1381 AGTTATTTCTGCTTCCAGTTTCTGATATTTTGTGATATTTAGATTTCTTGACTTATA 1440
QY 1441 TTTTGAATGGTCTTAGTGAAAGAAATGATATTTCTTTGAAGACATCGATATACATTT 1500
DB 1441 TTTTGAATGGTCTTAGTGAAAGAAATGATATTTCTTTGAAGACATCGATATACATTT 1500
QY 1501 ATTTACACTTTGATTTCTACATGTAAGAAATGAGGAAATGCCAATTTGATGTTGAT 1560
DB 1501 ATTTACACTTTGATTTCTACATGTAAGAAATGAGGAAATGCCAATTTGATGTTGAT 1560
QY 1561 AAAAGTCAGCTGAACCAAAAAAAGGAAATGAGGAAATGCCAATTTGATGTTGAT 1620
DB 1561 AAAAGTCAGCTGAACCAAAAAAAGGAAATGAGGAAATGCCAATTTGATGTTGAT 1620
QY 1621 A 1621
DB 1621 A 1621
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RESULT 5

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US-09-115-453-107
; Sequence 107, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-115-453-107

Query Match      100.0%; Score 1621; DB 3; Length 1621;
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACATGCACTGACAGGCACTCTCGGTATGAGCTGTCCGGCTCGGCCCGGGCCCGTT 60  
Db 1 GCACATGCACTGACAGGCACTCTCGGTATGAGCTGTCCGGCTCGGCCCGGGCCCGTT 60

Qy 61 CTGTGCTATGCTCTGCTGCTGCTCTCGGGCGGTGTGTAACGCTGAGACCGGCCGCTC 120  
Db 61 CTGTGCTATGCTCTGCTGCTGCTCTCGGGCGGTGTGTAACGCTGAGACCGGCCGCTC 120

Qy 121 CCGCTACCACTGAGCGCTTGGGCGGGGCAAGCGCTCGTGTGCTGAGACCTGCAAGCA 180  
Db 121 CCGCTACCACTGAGCGCTTGGGCGGGGCAAGCGCTCGTGTGCTGAGACCTGCAAGCA 180

Qy 181 GCGCGGGGAGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240  
Db 181 GCGCGGGGAGCGCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCC 240

Qy 241 CTTCGCGCGGTGTCTATGAGAACTCCAGCTGGGCCAGAGATTTCTGCAAGCGGAAAA 300  
Db 241 CTTCGCGCGGTGTCTATGAGAACTCCAGCTGGGCCAGAGATTTCTGCAAGCGGAAAA 300

Qy 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGTT 360  
Db 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGTT 360

Qy 361 AGCTGGCACAGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAG 420  
Db 361 AGCTGGCACAGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAG 420

Qy 421 TGGTGAGAACTCGTATGCGCGCTGAACTCTCTGCTGCTGCTGCTGCTGCTGCTTAT 480  
Db 421 TGGTGAGAACTCGTATGCGCGCTGAACTCTCTGCTGCTGCTGCTGCTGCTGCTTAT 480

Qy 481 GTGTGCTGCGCATTAATGCTCTTTTGGACCGCACGCACTGCAAGGGTFCAGGT 540  
Db 481 GTGTGCTGCGCATTAATGCTCTTTTGGACCGCACGCACTGCAAGGGTFCAGGT 540

Qy 541 CATTCATGCAAAATATGTTGGAAGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600  
Db 541 CATTCATGCAAAATATGTTGGAAGAACAGCATATTTAAGTCTTTCTGTGGAACCTCA 600

Qy 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAACTGTTGATGTTGAGACCTTTT 660  
Db 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAACTGTTGATGTTGAGACCTTTT 660

Qy 661 CTATAGGACTTACAGGACAGATGCGGGAATTCATGCTGTTGAGCAATAGAACCCCA 720  
Db 661 CTATAGGACTTACAGGACAGATGCGGGAATTCATGCTGTTGAGCAATAGAACCCCA 720

Qy 721 GTTCTACAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780  
Db 721 GTTCTACAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780

Qy 781 GAGCATGATGATTTGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGAAAGAC 840  
Db 781 GAGCATGATGATTTGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGAAAGAC 840

Qy 841 GAAGGACAGTGGTCAAACTTTTGAAGGACAGATGCTGTGCTGCTGCTGCTGCTGAC 900  
Db 841 GAAGGACAGTGGTCAAACTTTTGAAGGACAGATGCTGTGCTGCTGCTGCTGCTGAC 900

Qy 901 TTTTCAGGAGTGTGTTTCATGATGATCAAAAGGAAAGGGGCTCGTTTATCACCAGTGA 960  
Db 901 TTTTCAGGAGTGTGTTTCATGATGATCAAAAGGAAAGGGGCTCGTTTATCACCAGTGA 960

Qy 961 GGAGCAGGACGTGAGCGCCCGCTGCACTCTGCTGTTTAAACACCCCGCAGCATCCCTTC 1020  
Db 961 GGAGCAGGACGTGAGCGCCCGCTGCACTCTGCTGTTTAAACACCCCGCAGCATCCCTTC 1020

Qy 1021 TTTTCAAGGAGTCTTTTCATAGGAGAACACATGAGGAGTCTTGTGAGATTTGGATT 1080  
Db 1021 TTTTCAAGGAGTCTTTTCATAGGAGAACACATGAGGAGTCTTGTGAGATTTGGATT 1080

Db 1021 TTTTCAAGGAGTCTTTTCATAGGAGAACACATGAGGAGTCTTGTGAGAAATTTGGATT 1080  
Qy 1081 CAGCCGGAAGAGATTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAAATAGGTAAA 1140  
Db 1081 CAGCCGGAAGAGATTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAAATAGGTAAA 1140  
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Db 1201 TAGAGTAAACATAAATTTGATGCAATGGAACATGAGGAAACAGATTTACAGTGTCTTA 1260  
Qy 1261 CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320  
Db 1261 CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGATGATTTGAATTTCTAAA 1320  
Qy 1321 AATGGTTATCATTTAGGCTTTTGAATTTTATAAACTTTGGGTACTTATCTAAATTTATGGT 1380  
Db 1321 AATGGTTATCATTTAGGCTTTTGAATTTTATAAACTTTGGGTACTTATCTAAATTTATGGT 1380  
Qy 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTGATTTAAGATTTCTTGACTTTATA 1440  
Db 1381 AGTTATTTCTGCTTCCAGTTTGTGATATATTTTGTGATTTAAGATTTCTTGACTTTATA 1440  
Qy 1441 TTTTGAATGGTTCTAGTGAAAGAAATGATATTTCTTGAAGACATCGATATACATTTT 1500  
Db 1441 TTTTGAATGGTTCTAGTGAAAGAAATGATATTTCTTGAAGACATCGATATACATTTT 1500  
Qy 1501 ATTTACACTCTTGTATCTACAATGTAGAAAATGGAATGCGCAAAATTTGATGTTGAT 1560  
Db 1501 ATTTACACTCTTGTATCTACAATGTAGAAAATGGAATGCGCAAAATTTGATGTTGAT 1560  
Qy 1561 AAAAGTCAGCTGAAACAAAAAAGGAAATGGAATGGAATGGAATGGAATGGAATGGAAT 1620  
Db 1561 AAAAGTCAGCTGAAACAAAAAAGGAAATGGAATGGAATGGAATGGAATGGAATGGAAT 1620  
Qy 1621 A 1621  
Db 1621 A 1621

RESULT 6  
US-09-232-880-107  
; Sequence 107, Application US/09232880  
; Publication No. US20020182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.428C6  
; CURRENT APPLICATION NUMBER: US/09/232.880  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; US-09-232-880-107

Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACATGCACTGACAGGCACTCTCGGTATGAGCTGTCCGGCTCGGCCCGGGCCCGTT 60  
Db 1 GCACATGCACTGACAGGCACTCTCGGTATGAGCTGTCCGGCTCGGCCCGGGCCCGTT 60

Qy 61 CTGTGCTATGCTCTGCTGCTGCTCTCGGGCGGTGTGTAACGCTGAGACCGGCCGCTC 120



|||||  
Db CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGGTGTGGTACGCTGGAACGGGCCCGGCTC 120  
|||||  
Qy CGCTACGAGCTGAGCGGCTTGGGCGGGCAAGCGCTCGCTAGTCTGCTGACCTGAAGCA 180  
|||||  
Db CGCTACGAGCTGAGCGGCTTGGGCGGGCAAGCGCTCGCTAGTCTGCTGACCTGAAGCA 180  
|||||  
Qy GCGCGGGAGCGCGGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGCC 240  
|||||  
Db GCGCGGGAGCGCGGCTGCTGGCGGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGCC 240  
|||||  
Qy CTTCCCGCGGCTGCTCATGAGAGAACTCCAGCTGGGCCCGAGAGATTCTCAGCGGGAAAA 300  
|||||  
Db CTTCCCGCGGCTGCTCATGAGAGAACTCCAGCTGGGCCCGAGAGATTCTCAGCGGGAAAA 300  
|||||  
Qy TCCAGGCTATTATATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAGCTTCTGCGCGTT 360  
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Db TCCAGGCTATTATATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAGCTTCTGCGCGTT 360  
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Qy AGCTGCCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTGGCAGAAG 420  
|||||  
Db AGCTGCCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTGGCAGAAG 420  
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Qy TGGTGAAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTAT 480  
|||||  
Db TGGTGAAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTAT 480  
|||||  
Qy GTGTGACCTGGGCAATTATATGGCTCTTTTGAACGACACGACCTGACAAAGGGTCAGGT 540  
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Db GTGTGACCTGGGCAATTATATGGCTCTTTTGAACGACACGACCTGACAAAGGGTCAGGT 540  
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Qy CATTTGATCAAAATATGCTGGAAGAAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600  
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Db CATTTGATCAAAATATGCTGGAAGAAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600  
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Qy GAAATCAGCTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACCTTT 660  
|||||  
Db GAAATCAGCTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACCTTT 660  
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Qy CTATACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA 720  
|||||  
Db CTATACGACTTACAGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA 720  
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Qy GTTCTACGAGCTCTCATCAAGGACTTGAGCTAAAGTCTGATGAACCTTCCCAATCAGAT 780  
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Db GTTCTACGAGCTCTCATCAAGGACTTGAGCTAAAGTCTGATGAACCTTCCCAATCAGAT 780  
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Qy GAGCATGGATGATTGGCCAGAAATGAAGAAGATTTGCAGATGTTATTTGCAAAAGAAC 840  
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Db GAGCATGGATGATTGGCCAGAAATGAAGAAGATTTGCAGATGTTATTTGCAAAAGAAC 840  
|||||  
Qy GAAGGAGAGTGTGTCAAACTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900  
|||||  
Db GAAGGAGAGTGTGTCAAACTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900  
|||||  
Qy TTTTGAAGAGTGTTCATCATGATCAACACAGGAAACGGGCTCGTTTATCACCAGTCA 960  
|||||  
Db TTTTGAAGAGTGTTCATCATGATCAACACAGGAAACGGGCTCGTTTATCACCAGTCA 960  
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Qy GGAGGAGGAGCTGAGCGCCCGCTGCACCTCTGCTGTTAAACACCCCGAGCCATCCCTTC 1020  
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Db GGAGGAGGAGCTGAGCGCCCGCTGCACCTCTGCTGTTAAACACCCCGAGCCATCCCTTC 1020  
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Qy TTTCAAAAGGATTCCTTTATAGAGAAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080  
|||||  
Db TTTCAAAAGGATTCCTTTATAGAGAAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080  
|||||  
Qy CAGCCGGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAAATAGGTAAA 1140  
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Db CAGCCGGAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAAATAGGTAAA 1140  
|||||  
Qy AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAATAGTCTGATTTACAGTG 1200  
|||||

Db 1141 AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200  
Qy 1201 TAGAGTAACACATAACATTTGTATGATGAAACATGGAGAACAGTATTACAGTGTCCTA 1260  
Db 1201 TAGAGTAACACATAACATTTGTATGATGAAACATGGAGAACAGTATTACAGTGTCCTA 1260  
Qy 1261 CCACCTCTAATCAAGAAAAAATTACAGACTCTGATTCTTACAGTGATGATTGAATTTCTAAA 1320  
Db 1261 CCACCTCTAATCAAGAAAAAATTACAGACTCTGATTCTTACAGTGATGATTGAATTTCTAAA 1320  
Qy 1321 AATGGTTATCATTAGGGCTTTTGTATTAATAAACTTTGGGTACTTATACATAAATTTATGGT 1380  
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Qy 1381 AGTATTTCTCCCTCCAGTTTCTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1440  
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Db 1501 ATTTACACTCTTGATTCTTCAATGTAGAAAAATGAGAAATGCCACAAATTTGTATGGTAT 1560  
Qy 1561 AAAAGTCACGTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620  
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Qy 1621 A 1621  
Db 1621 A 1621

## RESULT 7

US-09-895-793-107  
; Sequence 107, Application US/09895793  
; Publication No. US20020192763A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuxiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Poy, Teresa  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C2  
; CURRENT APPLICATION NUMBER: US/09/895,793  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 1621  
; TYPE: DNA  
; ORGANISM: Homo sapien

US-09-895-793-107

Query Match		100.0%;	Score 1621;	DB 3;	Length 1621;		
Best Local Similarity		100.0%;	Pred. No. 0;				
Matches 1621;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	CGCCATGACACTGACAGGCACTCTGGTCATGAGCTGTCGGGCTGCGCCCTGGCCCGGCGCGTT	60				
Db	1	CGCCATGACACTGACAGGCACTCTGGTCATGAGCTGTCGGGCTGCGCCCGGCGCGTT	60				
Qy	61	CTGTGCTATGTCCTGCTGACTTCCGGCGCGCTGTGTAGCGGTGACCGCCCGGCTC	120				
Db	61	CTGTGCTATGTCCTGCTGACTTCCGGCGCGCTGTGTAGCGGTGACCGCCCGGCTC	120				
Qy	121	CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA	180				
Db	121	CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA	180				
Qy	181	GCCCGGGGAGCGCGCTGCTGCGGCGCTGTGCAAGCGGTGCGATGTGCTGGAGCC	240				
Db	181	GCCCGGGGAGCGCGCTGCTGCGGCGCTGTGCAAGCGGTGCGATGTGCTGGAGCC	240				
Qy	241	CTTCCGCGCGGTGTGTCAGTGAAGAACTCCAGCTGGGCGCAGAGATTCTGCAAGCGGAA	300				
Db	241	CTTCCGCGCGGTGTGTCAGTGAAGAACTCCAGCTGGGCGCAGAGATTCTGCAAGCGGAA	300				
Qy	301	TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTT	360				
Db	301	TCCAAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTT	360				
Qy	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGCGAGAG	420				
Db	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGCGAGAG	420				
Qy	421	TGCTGAGAAATCGTATGCCCCCTCAATCTCTGCTGCTGACTTTGCTGGTGGGCTTAT	480				
Db	421	TGCTGAGAAATCGTATGCCCCCTCAATCTCTGCTGCTGACTTTGCTGGTGGGCTTAT	480				
Qy	481	GTGTGACCTGGGCATTATTAATGGCTCTTTTGGCCGACAGCACTGCAAGGGTCAGGT	540				
Db	481	GTGTGACCTGGGCATTATTAATGGCTCTTTTGGCCGACAGCACTGCAAGGGTCAGGT	540				
Qy	541	CATTGATGCAATATGTTGGAGGAAACAGCATATTTAAGTCTTTCTGTGGAAACTCA	600				
Db	541	CATTGATGCAATATGTTGGAGGAAACAGCATATTTAAGTCTTTCTGTGGAAACTCA	600				
Qy	601	GAATCGAGTCTGTGGAGGACCTCGAGGACAGAACTGTTGGATGGTGAGACCTTT	660				
Db	601	GAATCGAGTCTGTGGAGGACCTCGAGGACAGAACTGTTGGATGGTGAGACCTTT	660				
Qy	661	CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720				
Db	661	CTATACGACTTACAGGACAGAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720				
Qy	721	GTTCACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATCCCAATCAGAT	780				
Db	721	GTTCACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATCCCAATCAGAT	780				
Qy	781	GAGCATGGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATTTTGAAGAAGAC	840				
Db	781	GAGCATGGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATTTTGAAGAAGAC	840				
Qy	841	GAAGGCAGAGTGGTGTCAAACTTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC	900				
Db	841	GAAGGCAGAGTGGTGTCAAACTTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC	900				
Qy	901	TTTTGAGGAGTGTTCATCATGATCAACAAGGAAACGGGCTCGTTTATCACCAGTGA	960				
Db	901	TTTTGAGGAGTGTTCATCATGATCAACAAGGAAACGGGCTCGTTTATCACCAGTGA	960				
Qy	961	GAGGAGGAGCGTGGAGCCCGGCTGACCTCTGCTGTTTAAACACCCAGGACCTCCCTC	1020				
Db	961	GAGGAGGAGCGTGGAGCCCGGCTGACCTCTGCTGTTTAAACACCCAGGACCTCCCTC	1020				

Qy	1021	TTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTTGAAGAAATTTGGATT	1080
Db	1021	TTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTTGAAGAAATTTGGATT	1080
Qy	1081	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA	1140
Db	1081	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAATAGGTAAA	1140
Qy	1141	AGCTAGTCTCTAACTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTCGATTTACAGTG	1200
Db	1141	AGCTAGTCTCTAACTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTCGATTTACAGTG	1200
Qy	1201	TAGAGTAACACATAACATTTGATGTCATGGAACATGCGAGAACAGTATTTACAGTGTCTA	1260
Db	1201	TAGAGTAACACATAACATTTGATGTCATGGAACATGCGAGAACAGTATTTACAGTGTCTA	1260
Qy	1261	CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTATGATTTGAAATTTCTAAA	1320
Db	1261	CCACTCTAAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTATGATTTGAAATTTCTAAA	1320
Qy	1321	AATGGTTATCATTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACATAATATGGT	1380
Db	1321	AATGGTTATCATTAGGCTTTTGAATTTATAAACTTTGGGTACTTATACATAATATGGT	1380
Qy	1381	AGTTATTTCTGGCTTCCAGTTTCTTGATATATTTGTTGATATTTAAAGATTTCTTGACTTATA	1440
Db	1381	AGTTATTTCTGGCTTCCAGTTTCTTGATATATTTGTTGATATTTAAAGATTTCTTGACTTATA	1440
Qy	1441	TTTTGAATGGTCTTCTAGTGAAGAAATGATATTTCTTTGAAGACATCGATATACATTT	1500
Db	1441	TTTTGAATGGTCTTCTAGTGAAGAAATGATATTTCTTTGAAGACATCGATATACATTT	1500
Qy	1501	ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTGAT	1560
Db	1501	ATTTACACTCTTGATTTCTCAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTGAT	1560
Qy	1561	AAAAAGTCAGTGAACAAAAAAGGAAATGATATTTCTTTGAAGACATCGATATACATTT	1620
Db	1561	AAAAAGTCAGTGAACAAAAAAGGAAATGATATTTCTTTGAAGACATCGATATACATTT	1620
Qy	1621	A 1621	
Db	1621	A 1621	

RESULT 8

US-09-895-814-107  
; Sequence 107, Application US/09895814  
; Publication No. US20020193296A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedrick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.





QY	661	CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTTTGGAGCAATAGAAACCCCA	720
Db	661	CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTTTGGAGCAATAGAAACCCCA	720
QY	721	GTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATCAACTTCCCAATCAGAT	780
Db	721	GTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATCAACTTCCCAATCAGAT	780
QY	781	GAGCATGGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAAAGAGAC	840
Db	781	GAGCATGGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAAAGAGAC	840
QY	841	GAAGGACAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGATCTCGGTTCTGAC	900
Db	841	GAAGGACAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGATCTCGGTTCTGAC	900
QY	901	TTTTGAGGAGGTTGTTTCATCATGATCAACAAGCAAGGAGGCTGCTTTATCACCAGTGA	960
Db	901	TTTTGAGGAGGTTGTTTCATCATGATCAACAAGCAAGGAGGCTGCTTTATCACCAGTGA	960
QY	961	GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC	1020
Db	961	GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTC	1020
QY	1021	TTTCAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATT	1080
Db	1021	TTTCAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGATTTGGATT	1080
QY	1081	CAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCAATGAAAGTAAATAGGTAAA	1140
Db	1081	CAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCAATGAAAGTAAATAGGTAAA	1140
QY	1141	AGCTAGTCTTAACTTTCAGGCGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG	1200
Db	1141	AGCTAGTCTTAACTTTCAGGCGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG	1200
QY	1201	TAGAGTAAACATAATTTGATGCATGAAACATGAGGAGAACAGTATTTACAGTGTCTTA	1260
Db	1201	TAGAGTAAACATAATTTGATGCATGAAACATGAGGAGAACAGTATTTACAGTGTCTTA	1260
QY	1261	CCACTCTAATCAAGAAAAGAAATACAGACTCTGATTTACAGTGTCTTAATTTCTTAAA	1320
Db	1261	CCACTCTAATCAAGAAAAGAAATACAGACTCTGATTTACAGTGTCTTAATTTCTTAAA	1320
QY	1321	AATGGTTATCATTTAGGGCTTTTGTATTAATAAACTTTGGGTACTTATCTAATAATTTGGT	1380
Db	1321	AATGGTTATCATTTAGGGCTTTTGTATTAATAAACTTTGGGTACTTATCTAATAATTTGGT	1380
QY	1381	AGTTATTTCTGCTTCCAGTTTGTGATPATATTTTGTGATATTAAGATTTCTGATTTATA	1440
Db	1381	AGTTATTTCTGCTTCCAGTTTGTGATPATATTTTGTGATATTAAGATTTCTGATTTATA	1440
QY	1441	TTTTGAATGGGTTCTAGTGAAGAAATGATATATTTCTTGAAGACATCGATATACATTT	1500
Db	1441	TTTTGAATGGGTTCTAGTGAAGAAATGATATATTTCTTGAAGACATCGATATACATTT	1500
QY	1501	ATTTACACTCTTGTATTTCTACAAATGAGAAATGAGGAAATGCCAAATTTGTATGGTGTAT	1560
Db	1501	ATTTACACTCTTGTATTTCTACAAATGAGAAATGAGGAAATGCCAAATTTGTATGGTGTAT	1560
QY	1561	AAAAAGTCAGTGAACAAAAAAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAAT	1620
Db	1561	AAAAAGTCAGTGAACAAAAAAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAAT	1620
QY	1621	A 1621	
Db	1621	A 1621	

Publication No. US20030088062A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang Yuqi

APPLICANT: Reed, Steven G.

APPLICANT: Kalos, Michael

APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark

APPLICANT: Solk, John

APPLICANT: Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1621; DB 6; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGCCATGGCACTGACAGGCAATCTGGTCTATGAGCTGTCGGGCTTGGCCCGGGCCGGTT	60
Db	1	CGCCATGGCACTGACAGGCAATCTGGTCTATGAGCTGTCGGGCTTGGCCCGGGCCGGTT	60
QY	61	CTGTGCTATGCTCTGGCTGACTTGGGGCGGCTGTGTGACGCTGACCGCGCGCTC	120
Db	61	CTGTGCTATGCTCTGGCTGACTTGGGGCGGCTGTGTGACGCTGACCGCGCGCTC	120
QY	121	CCGCTACGACGTGAGCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGGAAGCA	180
Db	121	CCGCTACGACGTGAGCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGGAAGCA	180
QY	181	GCGCGGGGAGCGCGCTGCTGGCGGCTGTGCAAGCGGTCGGATGCTGCTGGAGCC	240
Db	181	GCGCGGGGAGCGCGCTGCTGGCGGCTGTGCAAGCGGTCGGATGCTGCTGGAGCC	240
QY	241	CTTCCGCGGGGCTGATCGAGAACTCCAGCTGGGCGCCAGAGATTTGCAAGCGGAAA	300
Db	241	CTTCCGCGGGGCTGATCGAGAACTCCAGCTGGGCGCCAGAGATTTGCAAGCGGAAA	300
QY	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCCAGAACTTTCTGCGGTT	360
Db	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCCAGAACTTTCTGCGGTT	360
QY	361	AGCTGGCCACGATPATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAAATGGCAGAAG	420
Db	361	AGCTGGCCACGATPATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAAATGGCAGAAG	420
QY	421	TGTTGAGATCCGTATGCCCGCGCTGATCTCTGCTGCTGACTTTGCTGCTGCTTAT	480
Db	421	TGTTGAGATCCGTATGCCCGCGCTGATCTCTGCTGCTGACTTTGCTGCTGCTTAT	480
QY	481	GTGTGACCTGGGCAATTAATATGCTCTTTTTCACCGCACAGCACTGACAAAGGTCAGGT	540
Db	481	GTGTGACCTGGGCAATTAATATGCTCTTTTTCACCGCACAGCACTGACAAAGGTCAGGT	540
QY	541	CATTGATGCAAAATATGGTGGAGGAAACAGCATATTTAAAGTTCTTTCTGTGGAAAACTCA	600

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; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-144-678A-107

Query Match 100.0%; Score 1621; DB 7; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGCGACTGCAGGGCATCTCGGTCAATGGAGCTGTCGGGCTGCGGCCCTGGCCCCCGGGCCGGTT 60
Db 1 CGCCATGCGACTGCAGGGCATCTCGGTCAATGGAGCTGTCGGGCTGCGGCCCTGGCCCCCGGGCCGGTT 60

Qy 61 CTGTGCTATGTCCTGGCTGACTTCGCGGGCGGTGTGTGTACGCGTGGACCGCGCGGCTC 120
Db 61 CTGTGCTATGTCCTGGCTGACTTCGCGGGCGGTGTGTGTACGCGTGGACCGCGCGGCTC 120

Qy 121 CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCA 180
Db 121 CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCA 180

Qy 181 GCGCGGGGAGCCGCGTGTGCGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGGAGCC 240
Db 181 GCGCGGGGAGCCGCGTGTGCGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGGAGCC 240

Qy 241 CTTCCGCGCGGTGTGTCAGGAACTCCAGCTGGGCGCCAGAGATTCGACGCGGGA 300
Db 241 CTTCCGCGCGGTGTGTCAGGAACTCCAGCTGGGCGCCAGAGATTCGACGCGGGA 300

Qy 301 TCCAGGCTTATTTATGCGAGCTCAGTGGATTTCGCCAGTCAGGAAGCTTCTGCGGTT 360
Db 301 TCCAGGCTTATTTATGCGAGCTCAGTGGATTTCGCCAGTCAGGAAGCTTCTGCGGTT 360

Qy 361 AGCTGGCCAGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAAATTGGCAGAAG 420
Db 361 AGCTGGCCAGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAAATTGGCAGAAG 420

Qy 421 TGGTCAGAAATCCGATGCCCGCTCAATCTCCTGGCTGACTTTGCTGGTGGCCTTAT 480
Db 421 TGGTCAGAAATCCGATGCCCGCTCAATCTCCTGGCTGACTTTGCTGGTGGCCTTAT 480

421 TGGTGAGAAATCCGATGCCCGCTCAATCTCCTGGCTGACTTTGCTGGTGGCCTTAT 480
481 GTGTGACTGGGCAATTATATGCTCTTTTGGACCGCACAGCAGCTGACAGGGTCAGGT 540
481 GTGTGACTGGGCAATTATATGCTCTTTTGGACCGCACAGCAGCTGACAGGGTCAGGT 540
541 CATTGTGCAAAATATGTTGGAGGAAACAGCATATTTAAAGTCTCTTTCTGTGGAAAACTCA 600
541 CATTGTGCAAAATATGTTGGAGGAAACAGCATATTTAAAGTCTCTTTCTGTGGAAAACTCA 600
601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGACACTTTT 660
601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGACACTTTT 660
661 CTATACGACTTACAGGACAGCATGCGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
661 CTATACGACTTACAGGACAGCATGCGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
721 GTTCTACGAGCTGCTGATCAAGGACCTTGGACTTAAAGTCTGATGAACTTCCCAATCAGAT 780
721 GTTCTACGAGCTGCTGATCAAGGACCTTGGACTTAAAGTCTGATGAACTTCCCAATCAGAT 780
781 GAGCATGGATGATGGCCAGAAATGAAGAAAGTTTTGCAGATGTATTTTCCAAAGAAGAC 840
781 GAGCATGGATGATGGCCAGAAATGAAGAAAGTTTTGCAGATGTATTTTCCAAAGAAGAC 840
841 GAAGGACAGATGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCGGTTCTGAC 900
841 GAAGGACAGATGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCGGTTCTGAC 900
901 TTTTGGAGGCTTCTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
901 TTTTGGAGGCTTCTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGA 960
961 GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTTTAAACAACCCAGCCATCCCTTC 1020
961 GGAGCAGGACGTGAGCCCCCGCCCTGCACTCTGCTTTAAACAACCCAGCCATCCCTTC 1020
1021 TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGAGTT 1080
1021 TTTCAAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGAGTT 1080
1081 CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTCGAAAGTAAATAGGTAAA 1140
1081 CAGCCGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTCGAAAGTAAATAGGTAAA 1140
1141 AGCTAGTCTCTAACTTCCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200
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1201 TAGAGTAACACATAACTTGTATGTCATGGAAACATGAGGAGAACAGTATTACAGTGTCTTA 1260
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1261 CCACCTTAATCAAGAAAGAAATACAGACTCTGATTTCTACAGTGTGATTTCTTCTAAA 1320
1261 CCACCTTAATCAAGAAAGAAATACAGACTCTGATTTCTACAGTGTGATTTCTTCTAAA 1320
1321 AATGGTTATCATTTAGGCTTTTGAATTTTAAACCTTTGGGTACTTATATACTAAATATAGGT 1380
1321 AATGGTTATCATTTAGGCTTTTGAATTTTAAACCTTTGGGTACTTATATACTAAATATAGGT 1380
1381 AGTTATTTCTGCTTCCAGTTTCTTGAATATATTTTGTGATATTAAGATCTTGTGACTTATA 1440
1381 AGTTATTTCTGCTTCCAGTTTCTTGAATATATTTTGTGATATTAAGATCTTGTGACTTATA 1440
1441 TTTTGAATGGTCTTAGTGAAGAAAGGATGATATTTCTTGAAGACATCGATATACATTT 1500
1441 TTTTGAATGGTCTTAGTGAAGAAAGGATGATATTTCTTGAAGACATCGATATACATTT 1500
1501 ATTTTACACTCTTGTGATCTTACAAATGAGGAAATGAGGAAATGCCACAAATTTGTATGGTAT 1560
1501 ATTTTACACTCTTGTGATCTTACAAATGAGGAAATGAGGAAATGCCACAAATTTGTATGGTAT 1560
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```
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-234-786-107

Query Match 100.0%; Score 1621; DB 16; Length 1621;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCATGGCACTGCAAGGCACTCGGTGTCATGAGCTGTCGGCCCTGGCCCGGGCCCGGTT 60
Db 1 CGCCATGGCACTGCAAGGCACTCGGTGTCATGAGCTGTCGGCCCTGGCCCGGGCCCGGTT 60

Qy 61 CTGTGCTATGCTGCTGGCTGACTTCGGGGCGGTGTGTTACGCTGGACCGGCCCGGCTC 120
Db 61 CTGTGCTATGCTGCTGGCTGACTTCGGGGCGGTGTGTTACGCTGGACCGGCCCGGCTC 120

Qy 121 CCGCTACGACGTGAGCGGCTGCGGGCGGGAAGCGCTCGCTAGTGTGCTGACCTGAAGCA 180
Db 121 CCGCTACGACGTGAGCGGCTGCGGGCGGGAAGCGCTCGCTAGTGTGCTGACCTGAAGCA 180

Qy 181 GCCGGGGGAGCGCGGTGCTGCGGCTGCTGTGCAAGCGGTGCGATGCTGCTGAGCC 240
Db 181 GCCGGGGGAGCGCGGTGCTGCGGCTGCTGTGCAAGCGGTGCGATGCTGCTGAGCC 240

Qy 241 CTTCCGCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCGTCAGCGGGGAAA 300
Db 241 CTTCCGCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCGTCAGCGGGGAAA 300

Qy 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTT 360
Db 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCGGTT 360

361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAG 420
361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAG 420
421 TGGTGAGAAATCCGTATGCCCGCTGAAATCTCTCGCTGACTTTGCTGGTGGTGGCTTAT 480
421 TGGTGAGAAATCCGTATGCCCGCTGAAATCTCTCGCTGACTTTGCTGGTGGTGGCTTAT 480
481 GTGTGACTGGGCATTTAATAGGCTCTTTTGAACGCAACGCACTGACAGGGTCAAGT 540
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541 CATTGATGCAAAATATGGTGGAGGAAACAGCATATTTAAGTTCTTTCTGTGGAAGCACTCA 600
541 CATTGATGCAAAATATGGTGGAGGAAACAGCATATTTAAGTTCTTTCTGTGGAAGCACTCA 600
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661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
721 GTTCTACGAGCTGCTGATCAAGGACTTGGAGTAAAGTCTGATGAATTTCCCAATCAGAT 780
721 GTTCTACGAGCTGCTGATCAAGGACTTGGAGTAAAGTCTGATGAATTTCCCAATCAGAT 780
781 GAGCATGATGATTCGCCAGAAATCAAGAAAGTTCAGATGATTTTGAAGAAAGAC 840
781 GAGCATGATGATTCGCCAGAAATCAAGAAAGTTCAGATGATTTTGAAGAAAGAC 840
841 GAAAGCAGAGTGGTCAAAATCTTTGACGGCAACAGATGCTGTGACTCCGGTTCTGAC 900
841 GAAAGCAGAGTGGTCAAAATCTTTGACGGCAACAGATGCTGTGACTCCGGTTCTGAC 900
901 TTTTACGAGGTTGTTTCAATCATGATCAACAGGAAACGGGCTCGTTTATCACCAGTGA 960
901 TTTTACGAGGTTGTTTCAATCATGATCAACAGGAAACGGGCTCGTTTATCACCAGTGA 960
961 GAGCAGACGTCGAGCCCGCCCTGACCTCTGCTGTTTAAACACCCAGCCATCCCTTC 1020
961 GAGCAGACGTCGAGCCCGCCCTGACCTCTGCTGTTTAAACACCCAGCCATCCCTTC 1020
1021 TTTCAAAAGGATCCCTTTATAGGAGAAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
1021 TTTCAAAAGGATCCCTTTATAGGAGAAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080
1081 CAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAATCAATTTGAAGTAAATTAAGTAAA 1140
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1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATCTGCTTAAAGTAA 1200
1141 AGCTAGTCTCTAACTTCCAGGCCACCGCTCAAGTGAATTTGAATCTGCTTAAAGTAA 1200
1201 TAGAGTAAACATAAATTTGATGATGCAATGGAACATGAGGAGAAACAGTATTAAGTCTCTTA 1260
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1261 CCATCTTAATCAAGAAAGAAATTAAGTCTGATGATTTACAGTGAATTTGAATTTCTAAA 1320
1261 CCATCTTAATCAAGAAAGAAATTAAGTCTGATGATTTACAGTGAATTTGAATTTCTAAA 1320
1321 AATGGTATCAATAGGCTTTTGAATTAATAAACTTTGGTACTTATTAATAATTTATGTT 1380
1321 AATGGTATCAATAGGCTTTTGAATTTAATAAACTTTGGTACTTATTAATAATTTATGTT 1380
1381 AGTTATTTCTGCTTCCAGTTCGATGATATTTGCTGATATTAAGTTCCTGATTAATA 1440
1381 AGTTATTTCTGCTTCCAGTTCGATGATATTTGCTGATATTAAGTTCCTGATTAATA 1440
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Db	1381	AGTTATTCTTGCCTTCCAGTTTGGCTTGTGATATATTTTGTGATATTAAAGATTCTTGTGACTTATA	1444
Qy	1441	TTTTGAATGGGTCTCTAGTGAAGAAAGGAATGATATATTTCTTGAAGACATCCGATATACATTTT	1500
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Qy	1501	ATTTTACACTCTTTGATTCTTACAAATGTAGAAAAATGAGGAAATGCCACAAATTGTTATGGTGAT	1560
Db	1501	ATTTTACACTCTTTGATTCTTACAAATGTAGAAAAATGAGGAAATGCCACAAATTGTTATGGTGAT	1560
Qy	1561	AAAAGTACGCTGAACAAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1620
Db	1561	AAAAGTACGCTGAACAAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1620
Qy	1621	A 1621	
Db	1621	A 1621	
RESULT 15			
US-10-357-930-21284			
; Sequence 21284, Application US/10357930			
; Publication No. US20040259086A1			
; GENERAL INFORMATION:			
; APPLICANT: Schlengel, Robert			
; APPLICANT: Endege, Wilson			
; APPLICANT: Monahan, John			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
; TITLE OF INVENTION: HUMAN PROSTATE CANCER			
; FILE REFERENCE: MRI-007BCN			
; CURRENT APPLICATION NUMBER: US/10/357,930			
; CURRENT FILING DATE: 2003-02-04			
; PRIOR APPLICATION NUMBER: 09/785,276			
; PRIOR FILING DATE: 2003-02-16			
; PRIOR APPLICATION NUMBER: 60/183,319			
; PRIOR FILING DATE: 2000-02-17			
; PRIOR APPLICATION NUMBER: 60/189,862			
; PRIOR FILING DATE: 2000-03-16			
; PRIOR APPLICATION NUMBER: 60/207,454			
; PRIOR FILING DATE: 2000-05-25			
; PRIOR APPLICATION NUMBER: 60/211,314			
; PRIOR FILING DATE: 2000-06-09			
; PRIOR APPLICATION NUMBER: 60/219,007			
; PRIOR FILING DATE: 2000-07-18			
; PRIOR APPLICATION NUMBER: 60/255,281			
; PRIOR FILING DATE: 2000-12-13			
; NUMBER OF SEQ ID NOS: 62232			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 21284			
; LENGTH: 2376			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-357-930-21284			
Query Match 97.3%; Score 1577.4; DB 9; Length 2376;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1578; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	CGCCATGCACTGCAGGGCACTCTCGGTTCATGAGGCTGTCGGGCTTGGCCCGGCGCCGTTT	60
Db	97	CGCCATGCACTGCAGGGCACTCTCGGTTCATGAGGCTGTCGGGCTTGGCCCGGCGCCGTTT	156
Qy	61	CTGTGCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGATCGCTGGACCGGCGCCGCTC	120
Db	157	CTGTGCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGATCGCTGGACCGGCGCCGCTC	216
Qy	121	CCGCTACCACTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGCTGGACCTGAAGCA	180
Db	217	CCGCTACCACTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGCTGGACCTGAAGCA	276
Qy	181	GCCCGGGGAGCCGCGCTGCTGCGCGCTGTGTGCAAGCGGTCCGATGTGCTGCTGGAGCC	240

```
QY 1321 AATGGTTATCATAGGCTTTTGATTTATAAAACCTTTGGTACTTATCTAAATTTATGGT 1380
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1417 AATGGTTATCATAGGCTTTTGATTTATAAAACCTTTGGTACTTATCTAAATTTATGGT 1476
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1381 AGTTATCTGCCCTTCCAGTTTGGCTTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1440
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1477 AGTTATCTGCCCTTCCAGTTTGGCTTGATATATTTGTTGATATTAAGATTCTTGACTTATA 1536
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1441 TTTTGAATGGTTCTAGTGAAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1537 TTTTGAATGGTTCTAGTGAAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1596
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTGAT 1560
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1597 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTGAT 1656
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1561 AAAAGTCACGTGAACAAA 1579
Db |||||||||||||||
QY 1657 AAAAGTCACGTGAACAGA 1675
Db |||||||||||||||
```

Search completed: December 31, 2006, 13:56:06  
Job time : 2584.16 secs

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:07:59 ; Search time 1259.98 Seconds  
(without alignments)  
8969.963 Million cell updates/sec

Title: US-09-232-880-107  
Perfect score: 1621  
Sequence: 1 cccatggcactgcaggcca.....aaaaaaaaaaaaaaaaaaaaa 1621

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:  
14: geneseqn2005s:  
15: geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1621	100.0	1621	2	AAV58584 Prostate
2	1621	100.0	1621	2	AAV61199 Full leng
3	1621	100.0	1621	3	AAO06347 Human imm
4	1621	100.0	1621	3	ABS71252 Human pro
5	1621	100.0	1621	4	AAH93463 Human pro
6	1621	100.0	1621	4	AAH93463 Human pro
7	1621	100.0	1621	4	AAH02528 Prostate
8	1621	100.0	1621	4	AAH84777 Human pro
9	1621	100.0	1621	5	ACA59364 Prostate
10	1621	100.0	1621	5	AAH10106 Human pro
11	1621	100.0	1621	6	AB194927 Human Fl-
12	1621	100.0	1621	6	ABH58636 Prostate
13	1621	100.0	1621	8	ACC95091 Prostate
14	1621	100.0	1621	10	ADBI3557 Human pro
15	1621	100.0	1621	10	ADG26973 Human pro
16	1621	100.0	1621	15	Aef66254 Human pro
17	1577.4	97.3	2376	5	ABV25239 Human pro
18	1577.4	97.3	2376	5	ABV21293 Human pro

19	1577.4	97.3	2376	5	ABV21881 Human pro
20	1577.4	97.3	2376	5	ABV27112 Human pro
21	1575.8	97.2	1674	4	Aah13696 Human cDN
22	1575.8	97.2	2069	10	Adb75201 Prostate
23	1574.2	97.1	2005	6	ADB38607 Human alp
24	1574.2	97.1	2005	6	ADB38603 Human alp
25	1574.2	97.1	2005	10	ADD18532 Human pro
26	1574.2	97.1	2040	13	ACN38207 Tumour-as
27	1574.2	97.1	2069	6	ADB38604 Human alp
28	1574.2	97.1	2069	10	ADB75193 Prostate
29	1571	96.9	2534	15	AEE20414 Human AWA
30	1524.8	94.1	2068	6	ABK92152 Prostate
31	1524.8	94.1	2068	11	ADN39816 Cancer/an
32	1524.8	94.1	2068	12	ADP56740 Human alp
33	1524.8	94.1	2068	14	ADZ09628 Human bre
34	1245.4	76.8	2946	10	ADB75205 Prostate
35	1245.4	76.8	2946	12	ADP56742 Human alp
36	1243.8	76.7	3023	6	ADB38606 Human alp
37	1243.8	76.7	3023	10	ADB75197 Prostate
38	1134.4	70.0	2626	10	ADB75203 Prostate
39	1132.8	69.9	3654	6	ADB38605 Human alp
40	1132.8	69.9	3654	10	ADB75195 Prostate
41	940	58.0	1039	4	AAC91303 Human pol
42	903.6	55.7	1294	5	ABV22733 Human pro
43	903.6	55.7	1294	5	ABV28442 Human pro
44	903.6	55.7	1294	5	ABV28544 Human pro
45	903.6	55.7	1294	5	ABV22620 Human pro

## ALIGNMENTS

RESULT 1  
AAV58584  
ID AAV58584 standard; cDNA; 1621 BP.  
XX  
AC AAV58584;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-DEC-1998 (first entry)  
XX  
DE Prostate tumour specific gene clone Fl-12.  
XX  
KW Prostate tumour specific gene; human; prostate cancer; detection;  
KW therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 5..1153  
FT /tag= a  
XX  
PN WO9837418-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 25-FEB-1998; 98WO-US003690.  
XX  
PR 25-FEB-1997; 97US-00806596.  
PR 01-AUG-1997; 97US-00904809.  
PR 09-FEB-1998; 98US-00020747.  
XX  
(CORI-) CORIXA CORP.  
XX  
Xu J, Dillon DC;  
WPI: 1998-480805/41.  
P-PSDB; AAW69383.  
PT Novel human prostate specific tumour protein and fragments - useful for  
PT detecting and treating prostate cancers.  
XX  
PS Claim 1; Page 81-82; 141pp; English.





Query Match	Best Local Similarity	Mismatches	Conservative	Indels	Gaps	Other
1	CGCCATGGCACTGCAGGCGATCTCGGTCTATGGAGCTGTCCGGCTCGGCGCCCGGGCCCGTT	60	0	0	0	0
1	CGCCATGGCACTGCAGGCGATCTCGGTCTATGGAGCTGTCCGGCTCGGCGCCCGGGCCCGTT	60	0	0	0	0
61	CTGTGCTATGGTCTCGGTGACCTTTCGGGCGCGGTGTGGTACGCGTGGACCGCGCGGCTC	120	0	0	0	0
61	CTGTGCTATGGTCTCGGTGACCTTTCGGGCGCGGTGTGGTACGCGTGGACCGCGCGGCTC	120	0	0	0	0
121	CCGCTACGCTGAGCGGCTTGGGCGGCGGCAAGCGCTCGGTAGTGGACCTGGAAGCA	180	0	0	0	0
121	CCGCTACGCTGAGCGGCTTGGGCGGCGGCAAGCGCTCGGTAGTGGACCTGGAAGCA	180	0	0	0	0
181	GCCTGGGAGCGCGGCTGTGCGGCGCTGTGTCGAAGCGGTCCGATGTGCTGCGGAGCC	240	0	0	0	0



Db 1261 CCACCTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGATGATGAATTTCTAAA 1320  
Qy 1321 AATGGTTATCATTTAGGGCTTTTGGATTATATAAACTTTGGTACTTATACATAAATTATGTT 1380  
Db 1321 AATGGTTATCATTTAGGGCTTTTGGATTATATAAACTTTGGTACTTATACATAAATTATGTT 1380  
Qy 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTTGTGATATTTTGTGATATTTTGAATTTCTTGACTTATA 1440  
Db 1381 AGTTATTTCTGCTTCCAGTTTCTGATATATTTTGTGATATTTTGAATTTCTTGACTTATA 1440  
Qy 1441 TTTTGAATGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCATATATTTT 1500  
Db 1441 TTTTGAATGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCATATATTTT 1500  
Qy 1501 ATTTACACTCTTGATTTCTAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGTTGAT 1560  
Db 1501 ATTTACACTCTTGATTTCTAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGTTGAT 1560  
Qy 1561 AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620  
Db 1561 AAAAGTCACGTGAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1620  
Qy 1621 A 1621  
Db 1621 A 1621

RESULT 4  
ABS71252  
ID ABS71252 standard; cDNA; 1621 BP.  
XX AC ABS71252;  
XX DT 27-NOV-2002 (first entry) \*  
XX DE Human prostate tumour protein partial gene sequence #1.  
XX KW Human; immunogenic; prostate protein; prostate tumour protein;  
XX KW prostate cancer; cytostatic; vaccine; gene; ss.  
XX OS Homo sapiens.  
XX PN US2002090372-A1.  
XX PD 11-JUL-2002.  
XX PF 14-JUL-1998; 98US-00115453.  
XX PR 25-FEB-1997; 97US-00806099.  
XX PR 01-AUG-1997; 97US-00904804.  
XX PR 09-FEB-1998; 98US-00020956.  
XX PR 25-FEB-1998; 98US-00030607.  
XX (XUJJ/) XU J.  
XX (DILL/) DILLON D C.  
XX Xu J, Dillon DC;  
XX WPI; 2000-171268/15.  
XX P-PSDB; ABG94409.  
XX New polypeptide useful for treating and diagnosing prostate cancer  
XX comprises an immunogenic portion of prostate tumor protein.  
XX Claim 3; Page 54; 101pp; English.  
XX The present invention relates to a new polypeptide comprising an  
XX immunogenic portion of a prostate protein. The invention is useful for  
XX inhibiting the development of prostate cancer in a patient. The invention  
XX is also useful as markers for diagnosing prostate cancer and for  
XX monitoring diseases progression in patients. The present nucleic acid  
XX sequence represents a DNA sequence that is part of a gene encoding a  
XX human prostate tumour protein

XX SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1621; DB 3; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCCCATGGCACTCGACGGGCACTCTCGGTTCATGAGCTGTCCGGCTTGGCCCGGGCCCGTT 60  
Db 1 GCCCATGGCACTCGACGGGCACTCTCGGTTCATGAGCTGTCCGGCTTGGCCCGGGCCCGTT 60  
Qy 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGTACGCTGGAGCCGGCCCGGCTC 120  
Db 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGTGTGTACGCTGGAGCCGGCCCGGCTC 120  
Qy 121 CGCTTACGACGTGAGCCGCTTGGGGCGGGAAGGCTCGCTAGTGTCTGACCTGAAGCA 180  
Db 121 CGCTTACGACGTGAGCCGCTTGGGGCGGGAAGGCTCGCTAGTGTCTGACCTGAAGCA 180  
Qy 181 GCCGGGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGCGATGTCTGCTCGAGCC 240  
Db 181 GCCGGGGGAGCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGCGATGTCTGCTCGAGCC 240  
Qy 241 CTTCCCGCGGTGTCTATGAGAAACTCCAGCTGGGCCAGAGATTTGCGAGCGGAAAA 300  
Db 241 CTTCCCGCGGTGTCTATGAGAAACTCCAGCTGGGCCAGAGATTTGCGAGCGGAAAA 300  
Qy 301 TCCAAAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT 360  
Db 301 TCCAAAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT 360  
Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAAATGGCAGAG 420  
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAAATGGCAGAG 420  
Qy 421 TGGTGAGAAATCGTATGCCCGCTGAATCTCTCTGCTGCTGCTGCTGCTGCTGCTTAT 480  
Db 421 TGGTGAGAAATCGTATGCCCGCTGAATCTCTCTGCTGCTGCTGCTGCTGCTTAT 480  
Qy 481 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Qy 541 CATTTGATGCAAAATATGGTGAAGAAACAGCATATTTAAAGTCTCTTCTGTGAAAACTCA 600  
Db 541 CATTTGATGCAAAATATGGTGAAGAAACAGCATATTTAAAGTCTCTTCTGTGAAAACTCA 600  
Qy 601 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT 660  
Db 601 GAAATCGAGTCTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTT 660  
Qy 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGCAATAGAACCCCA 720  
Db 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGCAATAGAACCCCA 720  
Qy 721 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780  
Db 721 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGAT 780  
Qy 781 GAGCATGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTTTGGAAAAAGAAC 840  
Db 781 GAGCATGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTTTGGAAAAAGAAC 840  
Qy 841 GAGGCAGATGCTGCTCAAACTTTTGAAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGAC 900  
Db 841 GAGGCAGATGCTGCTCAAACTTTTGAAGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGAC 900  
Qy 901 TTTTTCAGGAGGTTGTTTCATCATGATCAAAAGGAAACGGGCTCGTTTATCACCAGTGA 960  
Db 901 TTTTTCAGGAGGTTGTTTCATCATGATCAAAAGGAAACGGGCTCGTTTATCACCAGTGA 960  
Qy 961 GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTTTAAACACCCCGCAGCATCCCTTC 1020  
Db 961 GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTTTAAACACCCCGCAGCATCCCTTC 1020

Db 961 GGAGCAGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCCGCCATCCCTTC 1020  
Qy 1021 TTTCAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTGGAAGAAATTTGGATT 1080  
Db 1021 TTTCAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATACCTTGGAAGAAATTTGGATT 1080  
Qy 1081 CAGCGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAATAGGTAAA 1140  
Db 1081 CAGCGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAATAGGTAAA 1140  
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCCCACGCTCAAGTGAATTTTGAATCTACGATTTACAGTG 1200  
Db 1141 AGCTAGTCTCTAACTTCCAGGCCCCACGCTCAAGTGAATTTTGAATCTACGATTTACAGTG 1200  
Qy 1201 TAGAGTAACACATAACATTTGATGATGGAACATGAGGAGAACAGTATTACAGTGTCTTA 1260  
Db 1201 TAGAGTAACACATAACATTTGATGATGGAACATGAGGAGAACAGTATTACAGTGTCTTA 1260  
Qy 1261 CCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTACAGTGATGATTTGAATTTCTAAA 1320  
Db 1261 CCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTACAGTGATGATTTGAATTTCTAAA 1320  
Qy 1321 AATGGTTATCATAGGGCTTTTGGATTTATATAAACTTTTGGTACTTTATATAAAATTTATGGT 1380  
Db 1321 AATGGTTATCATAGGGCTTTTGGATTTATATAAACTTTTGGTACTTTATATAAAATTTATGGT 1380  
Qy 1381 AGTTATCTGCTTCCAGTTTGTGATATATTTTGTGATATTAAGATTTCTGACTTATA 1440  
Db 1381 AGTTATCTGCTTCCAGTTTGTGATATATTTTGTGATATTAAGATTTCTGACTTATA 1440  
Qy 1441 TTTTGAATGGGTTCTAGTGAAAGAAAGGAATGATATATTTCTGAAGACATCGATATACATTT 1500  
Db 1441 TTTTGAATGGGTTCTAGTGAAAGAAAGGAATGATATATTTCTGAAGACATCGATATACATTT 1500  
Qy 1501 ATTTACACTCTTGATTTACAAATGAGAAATGAGAAATGCCAAATTTGTATGGTGAT 1560  
Db 1501 ATTTACACTCTTGATTTACAAATGAGAAATGAGAAATGCCAAATTTGTATGGTGAT 1560  
Qy 1561 AAAAGTCACGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620  
Db 1561 AAAAGTCACGTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620  
Qy 1621 A 1621  
Db 1621 A 1621

RESULT 5

AAH93463  
ID AAH93463 standard; cDNA; 1621 BP.

XX AC AAH93463;

XX DT 04-OCT-2001 (first entry)

XX DE Human prostate-specific full length cDNA sequence F1-12.

XX DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
KW cytosolic; gene therapy; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200151633-A2.

XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001574.

XX PR 14-JAN-2000; 2000US-00483672.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;  
PI Wang A, Meagher MJ;  
XX WPI; 2001-425873/45.  
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,  
PT monitoring and treating prostate cancer in a patient and for use in  
PT vaccines.  
XX Claim 1; Page 262-263; 543pp; English.  
XX The present invention describes polynucleotide sequences (I) which encode  
CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,  
CC and can be used in vaccine production and gene therapy. (I), (II),  
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells  
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and  
CC the antibodies are also used in the detection of cancer in a patient. The  
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)  
CC and (II) can be used in vaccines. The antibodies or (I) can be used for  
CC monitoring the progression of cancer in a patient. (I) and (II) can also  
CC be used to improve diagnostic and therapeutic methods for prostate  
CC cancer. They can indicate the level of metastasis as well as the prostate  
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent  
CC polynucleotide and amino acid sequences used in the exemplification of  
CC the present invention

SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match 100.0%; Score 1621; DB 4; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATGCGCATCTGCGGCGATCTCGGTCATGAGAGTCTCGGCGCTGCGCCCGCGCGCTT 60

Db 1 CGCATGCGCATCTGCGGCGATCTCGGTCATGAGAGTCTCGGCGCTGCGCCCGCGCGCTT 60

Qy 61 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db 61 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Qy 121 CCGCTACGACGTGAGCGCTTTGGCGCCGCGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCA 180

Db 121 CCGCTACGACGTGAGCGCTTTGGCGCCGCGGCAAGCGCTCGCTAGTGTGGACCTGGAAGCA 180

Qy 181 GCGCGGGAGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCT 240

Db 181 GCGCGGGAGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCT 240

Qy 241 CTTCCGCGCGGCTGCTCATGAGAACTCCAGCTGGGCGCCAGAGATTTCTGAGCGGGGAAAA 300

Db 241 CTTCCGCGCGGCTGCTCATGAGAACTCCAGCTGGGCGCCAGAGATTTCTGAGCGGGGAAAA 300

Qy 301 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTTCTGCCGGTT 360

Db 301 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTTCTGCCGGTT 360

Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTTGCTCTCAAAAATTTGCGAGAG 420

Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTTGCTCTCAAAAATTTGCGAGAG 420

Qy 421 TGGTGAGAAATCCGCTATGCCCGCTGGAATCTCTGGCTGACTTTTGGCTGGTGGCTTAT 480

Db 421 TGGTGAGAAATCCGCTATGCCCGCTGGAATCTCTGGCTGACTTTTGGCTGGTGGCTTAT 480

Qy 481 GTGTGCACTGGGCATTATTAATGGCTCTTTTGTAGCCGACACGCACTGACAGGCTCAGGT 540

Db 481 GTGTGCACTGGGCATTATTAATGGCTCTTTTGTAGCCGACACGCACTGACAGGCTCAGGT 540

Qy 541 CATTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600

Db 541 CATTGATGCAAAATATGTTGGAAGGAAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCA 600

Qy 601 GAAATCAGTCTGTGGGAAGCACCTCCGAGGACAGAAACATGTTGGATGTTGGAGCACCTTT 660

```
Db 601 GAAATCGAGTCTGTGGAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTT 660
Qy 661 CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Db 661 CTATACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Qy 721 GTTCTACGAGCTCTGATCAAGAGCACTTGAGCTAAAGTCTGATGAATCTCCCAATCAGAT 780
Db 721 GTTCTACGAGCTCTGATCAAGAGCACTTGAGCTAAAGTCTGATGAATCTCCCAATCAGAT 780
Qy 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAGAAGAC 840
Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCCAAGAAGAC 840
Qy 841 GAAGGACAGATGCTGTCTCAATCTTTGACGCCACAGATGCTGTGACTCCGGTCTTGAC 900
Db 841 GAAGGACAGATGCTGTCTCAATCTTTGACGCCACAGATGCTGTGACTCCGGTCTTGAC 900
Qy 901 TTTTGAAGGATGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGA 960
Db 901 TTTTGAAGGATGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGA 960
Qy 961 GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGGACGTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
Qy 1021 TTTCAAAAGGATCTTTATAGGAGAAACACTGAGGAGATCTTGAAGAAATTTGGATT 1080
Db 1021 TTTCAAAAGGATCTTTATAGGAGAAACACTGAGGAGATCTTGAAGAAATTTGGATT 1080
Qy 1081 CAGCCGAGAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAAGTAATAAGTAAA 1140
Db 1081 CAGCCGGAAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAAGTAATAAGTAAA 1140
Qy 1141 AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200
Qy 1201 TAGAGTAACACATAACATTTGATGATGGAACATGAGGAGACAGTATTTACAGTGTCTTA 1260
Db 1201 TAGAGTAACACATAACATTTGATGATGGAACATGAGGAGACAGTATTTACAGTGTCTTA 1260
Qy 1261 CCACTCTAATCAAGAAAGAAATACAGACTCTGATTTCTACAGTGATGATTTGAATCTTAA 1320
Db 1261 CCACTCTAATCAAGAAAGAAATACAGACTCTGATTTCTACAGTGATGATTTGAATCTTAA 1320
Qy 1321 AATGGTTATCATTTAGGGCTTTTGATTTATAAACTTTGGGTACTTATCTAAATTTATGTT 1380
Db 1321 AATGGTTATCATTTAGGGCTTTTGATTTATAAACTTTGGGTACTTATCTAAATTTATGTT 1380
Qy 1381 AGTTATCTGCTTCAGCTTTGCTGATATATTTGTTGATATTAAGATCTTGACTTATA 1440
Db 1381 AGTTATCTGCTTCAGCTTTGCTGATATATTTGTTGATATTAAGATCTTGACTTATA 1440
Qy 1441 TTTTGAATGGTCTAGTGAAGAAAGCAATATATTTCTGAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGTCTAGTGAAGAAAGCAATATATTTCTGAGACATCGATATACATTT 1500
Qy 1501 ATTTTACACTCTTGATTTCTACAATGTAGAAATGAGGAAATGCCACAAATTTGATGGTAT 1560
Db 1501 ATTTTACACTCTTGATTTCTACAATGTAGAAATGAGGAAATGCCACAAATTTGATGGTAT 1560
Qy 1561 AAAAGTCAGCTGAAA CAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 1620
Db 1561 AAAAGTCAGCTGAAA CAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621
```

RESULT 6

```
AAS63555
ID AAS63555 standard; cDNA; 1621 BP.
AC AAS63555;
XX 29-JAN-2002 (first entry)
XX Human prostate cDNA sequence #107.
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Homo sapiens.
XX WO200173032-A2.
XX 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US009919.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.
XX P-PSDB; AAU69761.
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
XX Claim 1; Page 264-265; 579pp; English.
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polynucleotide of the invention
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
Query Match 100.0%; Score 1621; DB 4; Length 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCCATGGCACTGACGGGCATCTCGGTTCATGGAGTGTCCGGCTTGGCCCGGCGCGT 60
Db 1 CGCCATGGCACTGACGGGCATCTCGGTTCATGGAGTGTCCGGCTTGGCCCGGCGCGT 60
Qy 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGCTGTGTGTACGCTGGACCGGCGGCTC 120
Db 61 CTGTGCTATGTCCTGGCTGACTTCGGGGCGGCTGTGTGTACGCTGGACCGGCGGCTC 120
Qy 121 CCGCTACGACGTGAGCCGCTTGGGCGGCAAGCGCTCGTCTAGTGTGCTGACCTGAAGCA 180
```



CC specific proteins and oligonucleotides that hybridise to a polynucleotide  
CC that encodes a prostate specific protein are useful for detecting the  
CC presence or absence of a cancer or monitoring the progression the  
CC progression of a cancer, especially prostate cancer. AA02422 to AA2872,  
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the  
CC exemplification of the present invention  
XX

SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match 100.0%; Score 1621; DB 4; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGGCACTGCAGGCGATCTCGGTCTATGGAGCTGTCGGGCTGGCCCGCCGGCCCGGT 60

DB 1 CGCCATGGCACTGCAGGCGATCTCGGTCTATGGAGCTGTCGGGCTGGCCCGCCGGCCCGGT 60

QY 61 CTGTGCTATGGTCTCGCTGACTTCGGGCGCGTGTGTACGCGTGGACCGGCGCGCTC 120

DB 61 CTGTGCTATGGTCTCGCTGACTTCGGGCGCGTGTGTACGCGTGGACCGGCGCGCTC 120

QY 121 CGCTACGAGCTGAGCGGCTTGGCCCGGGCAAGCGCTCGTAGTGTGACCTGAAGCA 180

DB 121 CGCTACGAGCTGAGCGGCTTGGCCCGGGCAAGCGCTCGTAGTGTGACCTGAAGCA 180

QY 181 GCGCGGGGAGCGCGCTGCTGGCGGCTGTGTGCAAGCGGTGCGATGCTGCGAGCC 240

DB 181 GCGCGGGGAGCGCGCTGCTGGCGGCTGTGTGCAAGCGGTGCGATGCTGCGAGCC 240

QY 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGGGAAA 300

DB 241 CTTCCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGGGAAA 300

QY 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGTT 360

DB 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGGCCAGTCAAGAGCTTCTGCCGTT 360

QY 361 AGTGCSCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAG 420

DB 361 AGTGCSCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAG 420

QY 421 TGGTGAGATCCGATATGCCCCGCTGAATCTCTGCGTGAATTTGCTGGTGGCCTTAT 480

DB 421 TGGTGAGATCCGATATGCCCCGCTGAATCTCTGCGTGAATTTGCTGGTGGCCTTAT 480

QY 481 GTGTGACCTGGGCAATTAATGGCTCTTTTGAAGCGCACGCACTGCAAGGTCAGGT 540

DB 481 GTGTGACCTGGGCAATTAATGGCTCTTTTGAAGCGCACGCACTGCAAGGTCAGGT 540

QY 541 CATTGATCAAAATATGCTGGAAGGACAGCATATTTAAGTCTTTTCTGGAAGACTCA 600

DB 541 CATTGATCAAAATATGCTGGAAGGACAGCATATTTAAGTCTTTTCTGGAAGACTCA 600

QY 601 GAAATCGAGTCTGTGGGAGCAGCTCCGAGCAGAACATGTTGGATGGGAGCAGCTTT 660

DB 601 GAAATCGAGTCTGTGGGAGCAGCTCCGAGCAGAACATGTTGGATGGGAGCAGCTTT 660

QY 661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATGAACCCCA 720

DB 661 CTATACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATGAACCCCA 720

QY 721 GTTCTACGAGCTGCTGATCAAGGACTTGGATTAAGTCTGATGACTTCCCAATCAGAT 780

DB 721 GTTCTACGAGCTGCTGATCAAGGACTTGGATTAAGTCTGATGACTTCCCAATCAGAT 780

QY 781 GAGCATGGATGATTTGCCAGAAATGAAGAAGATTTGCAGATGATTTTGCAGGAGAGAC 840

DB 781 GAGCATGGATGATTTGCCAGAAATGAAGAAGATTTGCAGATGATTTTGCAGGAGAGAC 840

QY 841 GAAGGCAGAGTGGTGTCAAACTTTTGAAGCGGACAGATGCTGTGTGACTCCGGTTCTGAC 900

DB 841 GAAGGCAGAGTGGTGTCAAACTTTTGAAGCGGACAGATGCTGTGTGACTCCGGTTCTGAC 900

QY 901 TTTTGGAGGAGTGTTCATCATGATCAACAAGAAACGGGCTCGTTTATCACCAGTGA 960

DB 901 TTTTGGAGGAGTGTTCATCATGATCAACAAGAAACGGGCTCGTTTATCACCAGTGA 960

QY 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCCGACCATCCCTTC 1020

DB 961 GGAGCAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCCGACCATCCCTTC 1020

QY 1021 TTTTAAAAAGGATCTTTTCATAGGAGAAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080

DB 1021 TTTTAAAAAGGATCTTTTCATAGGAGAAACACACTGAGGAGATCTTTGAAGAAATTTGGATT 1080

QY 1081 CAGCCGCGAAGAGATTTTATCAGCTTTAACTCAGATAAAATCATTTGAAAGTAATTAAGGTAAA 1140

DB 1081 CAGCCGCGAAGAGATTTTATCAGCTTTAACTCAGATAAAATCATTTGAAAGTAATTAAGGTAAA 1140

QY 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200

DB 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200

QY 1201 TAGAGTAACACATAAATTTGATGATGCAAAACATGGAGAACAGTATTACAGTGTCTTA 1260

DB 1201 TAGAGTAACACATAAATTTGATGATGCAAAACATGGAGAACAGTATTACAGTGTCTTA 1260

QY 1261 CCACCTCTAATCAAGAAAAAATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320

DB 1261 CCACCTCTAATCAAGAAAAAATTAACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320

QY 1321 AATGTTATCATTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATTAATTAATTTATGTT 1380

DB 1321 AATGTTATCATTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATTAATTAATTTATGTT 1380

QY 1381 AGTTATTTCTGCTCCAGTTTCTGATATATTTCTGATATTAAGATTTCTTGACTTATA 1440

DB 1381 AGTTATTTCTGCTCCAGTTTCTGATATATTTCTGATATTAAGATTTCTTGACTTATA 1440

QY 1441 TTTTCAATGGGTTCTAGTGAAAAAGAAATGATATATTTCTGAAGACATCGATATACATTT 1500

DB 1441 TTTTCAATGGGTTCTAGTGAAAAAGAAATGATATATTTCTGAAGACATCGATATACATTT 1500

QY 1501 ATTTACACTCTTGTATTTCTCAATGATGAAAAATGAGGAAATGCCAAATTTGATGTTGAT 1560

DB 1501 ATTTACACTCTTGTATTTCTCAATGATGAAAAATGAGGAAATGCCAAATTTGATGTTGAT 1560

QY 1561 AAAAGTCACTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620

DB 1561 AAAAGTCACTGAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620

QY 1621 A 1621

DB 1621 A 1621

RESULT 8

AAH84777

ID AAH84777 standard; cDNA; 1621 BP.

XX AAH84777;

XX 25-SEP-2001 (first entry)

XX Human prostate-specific cDNA sequence F1-12/P504S.

XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

XX chromosome 22q11.2; prostate-specific protein; chromosome 1;

XX prostate specific antigen; PSA; ss.

XX Homo sapiens.

XX WO200134802-A2.

XX 17-MAY-2001.

XX





Db 1621 A 1621

RESULT 9

ACAS9364

ID ACAS9364 standard; cDNA; 1621 BP.

XX AC ACAS9364;

XX 10-JUN-2003 (first entry)

XX Prostate cancer therapy associated cDNA #107.

XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;

KW immunogen; cancer; prostate specific antigen; PSA;

KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;

KW PSMA; gene; ss.

XX Homo sapiens.

XX OS

XX US2002192763-A1.

XX 19-DEC-2002.

XX 29-JUN-2001; 2001US-00895793.

XX 04-OCT-1999; 99US-0157455P.

PR 04-OCT-2000; 2000US-00679272.

PR 28-MAR-2001; 2001US-00822827.

XX (XUJ)/ XU J.

PA (DILL)/ DILLON D C.

PA (MITC)/ MITCHAM J L.

PA (HARL)/ HARLOCKER S L.

PA (JIAN)/ JIANG Y.

PA (KALO)/ KALOS M D.

PA (FANG)/ FANGER G R.

PA (RETT)/ RETTER M W.

PA (STOL)/ STOLK J A.

PA (DAYC)/ DAY C H.

PA (VEDV)/ VEDVICK T S.

PA (CART)/ CARTER D.

PA (LISX)/ LI S X.

PA (WANG)/ WANG A.

PA (SKEI)/ SKEIKY Y A W.

PA (HEPL)/ HEPLER W T.

PA (HEND)/ HENDERSON R A.

PA (HURA)/ HURAL J.

PA (MCNE)/ MCNEILL P D.

PA (HOUG)/ HOUGHTON R L.

PA (DBAS)/ Y DE BASSOLS C V.

PA (FOYT)/ FOY T M.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;

PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;

XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the

PT treatment and diagnosis of prostate cancer.

XX Example 1; SEQ ID NO 107; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino

CC acid sequence of immunogenic portions of any of the 3 sequences not

CC defined in the specification, or sequences having at least 70 or 90 %

CC sequence identity to any one of the 35 sequences defined in the USPTO web

CC site, which is encoded by any of the 4 nucleotide sequences not defined

CC in the specification. The fusion protein, composition and methods are

CC useful for diagnosing, preventing and/or treating cancer, particularly

CC prostate cancer. The proteins are useful as markers to indicate the

CC presence or absence of cancer. This sequence represents a prostate cancer

CC therapy associated cDNA. Note: The sequence data for this patent did not

CC form part of the printed specification, but was obtained in electronic

CC format directly from the US patent office at

CC seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX

XX Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match 100.0%; Score 1621; DB 5; Length 1621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCATGCGACCTGCGAGGCGATCTCGGTCTATGAGCTGTCCGGCTCGCCCGCCGGCCGCTT 60

DB 1 CGCCATGCGACCTGCGAGGCGATCTCGGTCTATGAGCTGTCCGGCTCGCCCGCCGGCCGCTT 60

QY 61 CTGTGCTATGGTCTCTGGCTGACTTTCGGGGCGGTGTGGTACGCGTGGACCGGCGCGGCTC 120

DB 61 CTGTGCTATGGTCTCTGGCTGACTTTCGGGGCGGTGTGGTACGCGTGGACCGGCGCGGCTC 120

QY 121 CGCTACGACCTGAGCGGCTTGGGCGGGGCAAGCGCTCGCTAGTCTGGAACCTGAAGCA 180

DB 121 CGCTACGACCTGAGCGGCTTGGGCGGGGCAAGCGCTCGCTAGTCTGGAACCTGAAGCA 180

QY 181 GCGCGGGGAGCGCGCTGCTGCGGCTCTGTGCAAGCGGTGCGATGTGCTGCTGAGCC 240

DB 181 GCGCGGGGAGCGCGCTGCTGCGGCTCTGTGCAAGCGGTGCGATGTGCTGCTGAGCC 240

QY 241 CTTCCGCCCGGTGTCTATGAGAAACTCCAGCTGGGCCAGAGATTTCTCAGCGGGA 300

DB 241 CTTCCGCCCGGTGTCTATGAGAAACTCCAGCTGGGCCAGAGATTTCTCAGCGGGA 300

QY 301 TCCAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAGCTTCTGCGGTT 360

DB 301 TCCAGGCTTATTTATGCCAGCTGAGTGGATTTGGCCAGTCAGGAGCTTCTGCGGTT 360

QY 361 AGCTGGCCACGATATCAACTATTGGCTTTGTTCAGGTGTCTCTCAAAAATTGGCAGAAG 420

DB 361 AGCTGGCCACGATATCAACTATTGGCTTTGTTCAGGTGTCTCTCAAAAATTGGCAGAAG 420

QY 421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCTGCGCTGACTTTGTGGTGGGCTTAT 480

DB 421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCTGCGCTGACTTTGTGGTGGGCTTAT 480

QY 481 GTGTGCACTGGGCAATTAATGGCTCTTTTTCACCGCACACGACTGCAAGGTCAGGT 540

DB 481 GTGTGCACTGGGCAATTAATGGCTCTTTTTCACCGCACACGACTGCAAGGTCAGGT 540

QY 541 CATTTGATGCAAAATATGGTGGAAAGAACAGCATATTTTAAAGTCTTTTCTGGAATACTCA 600

DB 541 CATTTGATGCAAAATATGGTGGAAAGAACAGCATATTTTAAAGTCTTTTCTGGAATACTCA 600

QY 601 GAAATCGAGTCTGTGGGAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACCTTT 660

DB 601 GAAATCGAGTCTGTGGGAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACCTTT 660

QY 661 CTATACGACTTACAGGACAGAGATGGGGAATTCATGGCTGTGGGCAATGAACCCCA 720

DB 661 CTATACGACTTACAGGACAGAGATGGGGAATTCATGGCTGTGGGCAATGAACCCCA 720

QY 721 GTTCTACGAGCTGTGATCAGAGGACTTGGAGCTTAAAGTCTGATGACTTCCCAATCAGAT 780

DB 721 GTTCTACGAGCTGTGATCAGAGGACTTGGAGCTTAAAGTCTGATGACTTCCCAATCAGAT 780

QY 781 GAGCATGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATATTTTGCAGGAGAC 840

DB 781 GAGCATGATGATGGCCAGAAATGAAGAAGTGTTCAGATGATATTTTGCAGGAGAC 840

QY 841 GAAGGAGAGTGGTCAAAATCTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900

DB 841 GAAGGAGAGTGGTCAAAATCTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGAC 900



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Qy 901 TTTTGAGAGGTTGTTGTCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGA 960
Db 901 TTTTGAGAGGTTGTTGTCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGA 960
Qy 961 GGAGCAGACGTGAGCCCGCCCTGCAACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
Db 961 GGAGCAGACGTGAGCCCGCCCTGCAACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
Qy 1021 TTTCAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT 1080
Db 1021 TTTCAAAGGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT 1080
Qy 1081 CAGCGCGAAGAGATTTATCAGCTTAACCTAGATAAATCAATTGAAGTAATAAGTAAA 1140
Db 1081 CAGCGCGAAGAGATTTATCAGCTTAACCTAGATAAATCAATTGAAGTAATAAGTAAA 1140
Qy 1141 AGCTAGTCTCTAACTCCAGGCCACAGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200
Db 1141 AGCTAGTCTCTAACTCCAGGCCACAGGCTCAAGTGAATTTGAATCTGCAATTTACAGTG 1200
Qy 1201 TAGAGTAACACATAACATTTGATGATGGAACATGAGGAACAGATATTACAGTGTCTTA 1260
Db 1201 TAGAGTAACACATAACATTTGATGATGGAACATGAGGAACAGATATTACAGTGTCTTA 1260
Qy 1261 CCACCTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTAATCTAAA 1320
Db 1261 CCACCTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTAATCTAAA 1320
Qy 1321 AATGGTTATCATTAAGGGCTTTTGATTTATAAACTTTGGGTACTTATATAAATTAATGGT 1380
Db 1321 AATGGTTATCATTAAGGGCTTTTGATTTATAAACTTTGGGTACTTATATAAATTAATGGT 1380
Qy 1381 AGTTATTCTGCTTCCAGCTTTGCTTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Db 1381 AGTTATTCTGCTTCCAGCTTTGCTTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440
Qy 1441 TTTTGAATGGGTTCTAGTGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Db 1441 TTTTGAATGGGTTCTAGTGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
Qy 1501 ATTTTACACTCTTGATTTCTACAAATGAGGAATGAGGAATGCCAAATTTGATGGTGAT 1560
Db 1501 ATTTTACACTCTTGATTTCTACAAATGAGGAATGAGGAATGCCAAATTTGATGGTGAT 1560
Qy 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620
Db 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620
Qy 1621 A 1621
Db 1621 A 1621
```

## RESULT 10

AAS10106  
ID AAS10106 standard; cDNA; 1621 BP.

XX  
AC AAS10106;

XX  
DT 24-OCT-2001 (first entry)

XX  
DE Human prostate tumour cDNA F1-12 #3.

XX  
KW Human; prostate tumour protein; prostate cancer; ss.

XX  
OS Homo sapiens.

XX  
PN US6262245-B1.

XX  
PD 17-JUL-2001.

XX  
PF 25-FEB-1998; 98US-00030607.

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PR 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 09-FEB-1998; 98US-00020956.  
XX (CORI-) CORIXA CORP.  
XX  
XX Xu J, Dillon DC;  
PI  
XX WPI; 2001-440862/47.  
DR P-PSDB; AAU04959.  
XX  
PT Novel polynucleotide encoding polypeptide comprising a portion of  
PT prostate tumor protein useful for inhibiting development of prostate  
PT cancer or for treating prostate cancer in a patient.  
XX  
XX Claim 1; Col 112-113; 105pp; English.  
XX  
XX The sequence is a human prostate tumour cDNA which encodes a partial  
CC tumour protein. The DNA is useful for inhibiting the development of  
CC prostate cancer or for treating prostate cancer in a patient  
XX  
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1621; DB 5; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGCATGGCACTCGAGGGCATCTCGTTCATGGAGCTGTCGGGCTGCCCCGGGCCCGTT 60  
Db 1 CGCATGGCACTCGAGGGCATCTCGTTCATGGAGCTGTCGGGCTGCCCCGGGCCCGTT 60  
Qy 61 CTGTGCTATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Db 61 CTGTGCTATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
Qy 121 CCGCTACAGCTGAGCGCTTTGGCCGGGGCAAGCGCTCGCTAGTGTGCACTGGAAGCA 180  
Db 121 CCGCTACAGCTGAGCGCTTTGGCCGGGGCAAGCGCTCGCTAGTGTGCACTGGAAGCA 180  
Qy 181 GCCCGGGGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
Db 181 GCCCGGGGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
Qy 241 CTTCCCGCGGGTGTCTCATGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGAGCGGGA 300  
Db 241 CTTCCCGCGGGTGTCTCATGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGAGCGGGA 300  
Qy 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCCGGTT 360  
Db 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAAAGCTTCTGCCGGTT 360  
Qy 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGCGAGA 420  
Db 361 AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGCGAGA 420  
Qy 421 TGGTGAGAAATCCGATGCCCGCTGAATCTCCTGGCTGACTTTTCTGGTGGTGGCTTAT 480  
Db 421 TGGTGAGAAATCCGATGCCCGCTGAATCTCCTGGCTGACTTTTCTGGTGGTGGCTTAT 480  
Qy 481 GTGTGCACCTGGGCATTTAATATGCTCTTTTGACCCGACACGCACTGCAAGGCTCAGGT 540  
Db 481 GTGTGCACCTGGGCATTTAATATGCTCTTTTGACCCGACACGCACTGCAAGGCTCAGGT 540  
Qy 541 CATTGATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCA 600  
Db 541 CATTGATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCA 600  
Qy 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGGACCTTT 660  
Db 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGGACCTTT 660  
Qy 661 CTATACGACTTACAGGACAGCATGGGAATTCATGGCTGTTTGGAGCAATAGAACCCCA 720  
Db 661 CTATACGACTTACAGGACAGCATGGGAATTCATGGCTGTTTGGAGCAATAGAACCCCA 720
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Db 661 CTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTGGAGCAATGAACCCCA 720  
Qy 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAGAGTCTGATGAACCTCCCAATCAGAT 780  
Db 721 GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAGAGTCTGATGAACCTCCCAATCAGAT 780  
Qy 781 GAGCATGGATGATTTGGCCAGAAATGAAGAAGAAATTTGAGATGATTTGCAAAAGAGAC 840  
Db 781 GAGCATGGATGATTTGGCCAGAAATGAAGAAGAAATTTGAGATGATTTGCAAAAGAGAC 840  
Qy 841 GAAGGAGAGTGTGTCAAACTTTTGAAGGACAGATGCTGTGTGACTCCGGTTCTGAC 900  
Db 841 GAAGGAGAGTGTGTCAAACTTTTGAAGGACAGATGCTGTGTGACTCCGGTTCTGAC 900  
Qy 901 TTTTGAAGGATTTTTCATCATCATCATCAACAAGGAAACGGGCTCGTTTATCACCACTGA 960  
Db 901 TTTTGAAGGATTTTTCATCATCATCATCAACAAGGAAACGGGCTCGTTTATCACCACTGA 960  
Qy 961 GGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020  
Db 961 GGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020  
Qy 1021 TTTCAAAAGGATCTTTTATAGGAGAAACACCTGAGGAGATCTGTAAGAAATTTGGATT 1080  
Db 1021 TTTCAAAAGGATCTTTTATAGGAGAAACACCTGAGGAGATCTGTAAGAAATTTGGATT 1080  
Qy 1081 CAGCCGCGAGAGATTTATCAGCTTAACCTGAGATAAATCAATGAAGTAATAAGTAA 1140  
Db 1081 CAGCCGCGAGAGATTTATCAGCTTAACCTGAGATAAATCAATGAAGTAATAAGTAA 1140  
Qy 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200  
Db 1141 AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAAATCTGCAATTTACAGTG 1200  
Qy 1201 TAGAGTAACACATAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
Db 1201 TAGAGTAACACATAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
Qy 1261 CCACCTCTAATCAGAAAGAAATACAGACTCTGATTTCTACAGTGAATGATGATGATGATGAT 1320  
Db 1261 CCACCTCTAATCAGAAAGAAATACAGACTCTGATTTCTACAGTGAATGATGATGATGATGAT 1320  
Qy 1321 AATGGTTATCATTTAGGCTTTTGAATTTATAAAACTTTGGTACTTACTTAAATTAATGAT 1380  
Db 1321 AATGGTTATCATTTAGGCTTTTGAATTTATAAAACTTTGGTACTTACTTAAATTAATGAT 1380  
Qy 1381 AGTTATCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440  
Db 1381 AGTTATCTGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440  
Qy 1441 TTTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATGATATACATTT 1500  
Db 1441 TTTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATGATATACATTT 1500  
Qy 1501 ATTTACACTCTTGAATTTCAATGTAAGAAATGAGGAAATGCCAATTTGATGATGAT 1560  
Db 1501 ATTTACACTCTTGAATTTCAATGTAAGAAATGAGGAAATGCCAATTTGATGATGAT 1560  
Qy 1561 AAAAGTCAGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620  
Db 1561 AAAAGTCAGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1620  
Qy 1621 A 1621  
Db 1621 A 1621

## RESULT 11

ABU94927  
ID ABL94927 standard; cDNA; 1621 BP.

XX ABL94927;

AC ABL94927;

XX ABL94927;

DT 19-JUL-2002 (first entry)  
XX Human FI-12 cDNA sequence SEQ ID NO 107.  
DE Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;  
XX gene therapy; gene; ss.  
KW Homo sapiens.  
XX OS  
XX PN US2002022248-A1.  
XX 21-FEB-2002.  
XX 12-JAN-2001; 2001US-00759143.  
XX 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 10-FEB-1998; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
PR 14-JUL-1998; 98US-00115453.  
PR 23-SEP-1998; 98US-00159812.  
PR 15-JAN-1999; 99US-00232149.  
PR 09-APR-1999; 99US-00288946.  
PR 13-JUL-1999; 99US-00352616.  
PR 12-NOV-1999; 99US-00439313.  
PR 18-NOV-1999; 99US-00443686.  
PR 14-JAN-2000; 2000US-00483672.  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PR 12-MAY-2000; 2000US-00570737.  
PR 13-JUN-2000; 2000US-00593793.  
PR 27-JUN-2000; 2000US-00605783.  
PR 10-AUG-2000; 2000US-00636215.  
PR 29-AUG-2000; 2000US-00651236.  
PR 06-SEP-2000; 2000US-00657279.  
PR 02-OCT-2000; 2000US-00679426.  
PR 10-OCT-2000; 2000US-00685166.  
XX (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (REIT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
WPI; 2002-255649/30.  
XX New prostate-specific polynucleotides for diagnosing and treating  
PT diseases, in particular prostate cancer, and as markers for the  
PT progression of cancer.  
XX Claim 1; SEQ ID NO 107; 87pp; English.  
PS The present invention provides prostate-specific coding sequences and  
XX their encoded proteins. These can be used in the diagnosis and treatment  
CC of cancers, particularly prostate cancer. The present sequence is a cDNA  
CC described in the invention  
XX







Db 1381 AGTTATTCCTCCCTTCCGTTTGGCTTGATATATATTTGTTGATATTAAGATTCTTGACTTATA 1440  
QY 1441 TTTTGAATGGTTCTAGTGAAGAAAGGAATCATATATTTCTTGAAGACATCGATATACATTT 1500  
Db 1441 TTTTGAATGGTTCTAGTGAAGAAAGGAATCATATATTTCTTGAAGACATCGATATACATTT 1500  
QY 1501 ATTTACACTCTTGATTTCTACAAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTAT 1560  
Db 1501 ATTTACACTCTTGATTTCTACAAATGTAGAAAATGAGGAAATGCCACAAATTTGTATGGTAT 1560  
QY 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620  
Db 1561 AAAAGTCACGTGAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1620  
QY 1621 A 1621  
Db 1621 A 1621  
RESULT 14  
ADBI3557  
ID ADBI3557 standard; cDNA; 1621 BP.  
XX AC ADBI3557;  
XX DT 18-DEC-2003 (first entry)  
XX DE Human prostate specific full length cDNA F1-12/P504S.  
XX KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;  
KW gene therapy; cell therapy; vaccine; T-cell epitope;  
KW class I major histocompatibility complex allele; MHC; prostate cancer;  
KW tumour; antigen presenting cell.  
XX OS Homo sapiens.  
XX PN US2003185830-A1.  
XX PD 02-OCT-2003.  
XX PF 12-NOV-2002; 2002US-00294025.  
XX PR 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 09-FEB-1998; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
PR 14-JUL-1998; 98US-00115453.  
PR 23-SEP-1998; 98US-00159812.  
PR 15-JAN-1999; 99US-00232149.  
PR 09-APR-1999; 99US-00288946.  
PR 13-JUL-1999; 99US-00352616.  
PR 12-NOV-1999; 99US-00439313.  
PR 18-NOV-1999; 99US-00443686.  
PR 14-JAN-2000; 2000US-00483672.  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PR 12-MAY-2000; 2000US-00570737.  
PR 13-JUN-2000; 2000US-00593793.  
PR 27-JUN-2000; 2000US-00605783.  
PR 09-AUG-2000; 2000US-00636215.  
PR 29-AUG-2000; 2000US-00651236.  
PR 06-SEP-2000; 2000US-00657279.  
PR 02-OCT-2000; 2000US-00679426.  
PR 10-OCT-2000; 2000US-00685166.  
PR 09-NOV-2000; 2000US-00709729.  
PR 12-JAN-2001; 2001US-00759143.  
PR 09-FEB-2001; 2001US-00780669.  
PR 09-MAY-2001; 2001US-00852911.  
PR 29-JUN-2001; 2001US-00895814.  
PR 10-DEC-2001; 2001US-00912896.  
PR 09-MAY-2002; 2002US-00144678.  
XX (CORI-) CORIXA CORP.  
PA

XX Xu J, Stolk JA, Kalos MD;  
PI WPI: 2003-756193/71.  
DR P-PSDB; ADBI3558.  
XX New isolated polypeptide for use in a vaccine for stimulating an immune  
PT response, or for treating or diagnosis cancer, preferably prostate  
PT cancer.  
XX Claim 19; Page; 101pp; English.  
PS The invention relates to an isolated polypeptide comprising no more than  
XX 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The  
CC peptides comprise a fragment ADBI3563 of that contain naturally processed  
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)  
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific  
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids  
CC encoding the proteins and peptides, expression vectors, a host cell  
CC transformed with the vector, an isolated antibody (or antigen binding  
CC fragment) that specifically binds to the protein or peptide, detecting  
CC the presence of a cancer in a patient (comprising contacting a patient  
CC sample with a binding agent that binds to the peptides or a polypeptide  
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to  
CC the agent and comparing the amount of polypeptide to a predetermined cut-  
CC off value to determine the presence of cancer), a fusion protein  
CC comprising the peptides or proteins, stimulating or expanding T cells  
CC specific for a tumour protein comprising contacting T cells with the  
CC peptides or the isolated T cell population, treating prostate cancer in a  
CC patient comprising administering a composition comprising the peptides,  
CC nucleic acids, antibodies or compounds, determining the presence of a  
CC cancer in a patient and treating prostate cancer in a patient comprising  
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated  
CC from a patient with the peptides or antigen presenting cells that express  
CC (the peptides so that the T cells proliferate, and administering the  
CC proliferated T cells to the patient. The peptides (or an oligonucleotide  
CC that hybridises to nucleic acid encoding them), is used to detect the  
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or  
CC antigen-presenting cells expressing the nucleic acid, are used to  
CC stimulate or expand T cells specific for a tumour protein. The peptides,  
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen  
CC presenting cells are used to stimulate an immune response or treat  
CC prostate cancer in a patient. The present sequence is one of the  
CC disclosed human prostate specific cDNAs. Note: Except where otherwise  
CC indicated, the sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html?docID=20030185830](http://seqdata.uspto.gov/sequence.html?docID=20030185830).  
XX Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 1621; DB 10; Length 1621;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGCCATGGCAGTCGAGGGCATCTCGGTCTATGAGCTGTCCGGCTTGGCCCGCCCGCCGTT 60  
Db 1 CGCCATGGCAGTCGAGGGCATCTCGGTCTATGAGCTGTCCGGCTTGGCCCGCCCGCCGTT 60  
QY 61 CTGTGCTATGTCCTGGTGTGACTTCGGGGCGCGTGTGTGTACGCGTGGACCGCCCGGCTC 120  
Db 61 CTGTGCTATGTCCTGGTGTGACTTCGGGGCGCGTGTGTGTACGCGTGGACCGCCCGGCTC 120  
QY 121 CGGCTACGACGTGACCGCTTGGGGCGGGGCGGAGCGCTCGCTAGTCTGGACCTGAGCA 180  
Db 121 CGGCTACGACGTGACCGCTTGGGGCGGGGCGGAGCGCTCGCTAGTCTGGACCTGAGCA 180  
QY 181 GCGCGGGGAGCGCCGCTGTCTGCGCGCTCTGTGCAAGCGGTGCGATGTCTGCTGAGCC 240  
Db 181 GCGCGGGGAGCGCCGCTGTCTGCGCGCTCTGTGCAAGCGGTGCGATGTCTGCTGAGCC 240  
QY 241 CTTCCGCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGACGGGAAA 300  
Db 241 CTTCCGCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGACGGGAAA 300





PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvik TS;  
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;  
PI Meagher MJ, Deng T;  
XX WPI; 2003-777973/73.  
DR P-PSDB; ADG25974.  
XX  
PT New polynucleotides encoding prostate specific polypeptides isolated from  
PT a human prostate tumor cDNA library are useful to diagnose and treat  
PT cancer particularly prostate cancer.  
XX  
PS Example 1; SEQ ID NO 107; 99pp; English.  
PS  
XX The invention relates to human prostate-specific polypeptides and the  
CC polynucleotides encoding them. The invention also relates to an isolated  
CC antibody or its antigen-binding fragment that specifically binds a  
CC polypeptide of the invention, a method of detecting cancer in a patient  
CC comprising contacting a biological sample of the patient with an agent  
CC that binds a prostate-specific polypeptide and comparing the amount of  
CC bound polypeptide compared to a predetermined cut-off value and a fusion  
CC protein comprising a prostate-specific polypeptide. The sequences of the  
CC invention are used to diagnose and treat cancer, particularly prostate  
CC cancer. This sequence represents cDNA encoding a human prostate-specific  
CC polypeptide of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification but was obtained in electronic  
CC format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;  
  
Query Match  
Best Local Similarity 100.0%; Score 1621; DB 10; Length 1621;  
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGCCATGGCACTGCAGGGCATCTCGGTCTATGGAGTGTCCGCCCTGGCCCGGGCCGGTT 60  
DB 1 CGCCATGGCACTGCAGGGCATCTCGGTCTATGGAGTGTCCGCCCTGGCCCGGGCCGGTT 60  
  
QY 61 CTGTGCTATGGTCTGGCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGCCGGCTC 120  
DB 61 CTGTGCTATGGTCTGGCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGCCGGCTC 120  
  
QY 121 CGCTACGACGTGAGCGGCTTGGCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180  
DB 121 CGCTACGACGTGAGCGGCTTGGCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCA 180  
  
QY 181 GCGCGGGGAGCGCGGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCC 240  
DB 181 GCGCGGGGAGCGCGGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCC 240  
  
QY 241 CTTTCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGACGGGGAAA 300  
DB 241 CTTTCGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCGACGGGGAAA 300  
  
QY 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGCGCAGTCAGAGCTTCGCGGTT 360  
DB 301 TCCAGGCTTATTTATGCGAGCTGAGTGGATTTGCGCAGTCAGAGCTTCGCGGTT 360  
  
QY 361 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTGTCTCATAAAATTTGGCAGAAG 420  
DB 361 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTGTCTCATAAAATTTGGCAGAAG 420  
  
QY 421 TGGTGAGAAATCGGTATGCGCCCGTGAATCTCTGCTGACTTTGCTGGTGGCTTAT 480  
DB 421 TGGTGAGAAATCGGTATGCGCCCGTGAATCTCTGCTGACTTTGCTGGTGGCTTAT 480  
  
QY 481 GTGTGCACTGGCATTATATCGCTTTTTCACCGCACCGCACTGCAAGGGTCAGGT 540  
DB 481 GTGTGCACTGGCATTATATCGCTTTTTCACCGCACCGCACTGCAAGGGTCAGGT 540  
  
QY 541 CATTGATGCAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGTGGAAACTCA 600  
DB 541 CATTGATGCAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGTGGAAACTCA 600

DB 541 CATTGATGCAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGTGGAAACTCA 600  
QY 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGTGTGGACACCTTT 660  
DB 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGTGTGGACACCTTT 660  
QY 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGTGGAGCAATAGAACCCCA 720  
DB 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGTGGAGCAATAGAACCCCA 720  
QY 721 GTTCTACAGCTGTGATCAAGGACCTTGGGAAAGTCTGATGAACCTCCCAATCAGAT 780  
DB 721 GTTCTACAGCTGTGATCAAGGACCTTGGGAAAGTCTGATGAACCTCCCAATCAGAT 780  
QY 781 GAGCATGATGATGGCCAGAAATGAAGAAGTTCAGATGTATTTGCAAGAAGAC 840  
DB 781 GAGCATGATGATGGCCAGAAATGAAGAAGTTCAGATGTATTTGCAAGAAGAC 840  
QY 841 GAAGCAGAGTGTGTCAAAATCTTTTGACGGCACAGATCCCTGTGTGACTCCGGTTCTGAC 900  
DB 841 GAAGCAGAGTGTGTCAAAATCTTTTGACGGCACAGATCCCTGTGTGACTCCGGTTCTGAC 900  
QY 901 TTTTGAGGAGTGTGTTCATCATGTATCAACAAGGAACGGGGCTCGTTATCACAGTGA 960  
DB 901 TTTTGAGGAGTGTGTTCATCATGTATCAACAAGGAACGGGGCTCGTTATCACAGTGA 960  
QY 961 GGAGCAGACCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020  
DB 961 GGAGCAGACCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020  
QY 1021 TTTCAAAAGGGATCCTTTTCATAGGAGAACACATGAGGAGTACTTTGAAGATTTGGATT 1080  
DB 1021 TTTCAAAAGGGATCCTTTTCATAGGAGAACACATGAGGAGTACTTTGAAGATTTGGATT 1080  
QY 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAGGTAAA 1140  
DB 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAGGTAAA 1140  
QY 1141 AGCTAGTCTCTAACTTCCAGGCCCAAGTCAAGTGAATTTGAATCTGATGCTTACAGTG 1200  
DB 1141 AGCTAGTCTCTAACTTCCAGGCCCAAGTGAATTTGAATCTGATGCTTACAGTG 1200  
QY 1201 TAGAGTAACACATAACATTTGATGATGGAACCAATGAGGAGAACAGTATTAACAGTCTCTA 1260  
DB 1201 TAGAGTAACACATAACATTTGATGATGGAACCAATGAGGAGAACAGTATTAACAGTCTCTA 1260  
QY 1261 CCACTCTAATCAAGAAAGAAATTAACAGCTCTGATTTCTACAGTGAATGAAATTTCTAAA 1320  
DB 1261 CCACTCTAATCAAGAAAGAAATTAACAGCTCTGATTTCTACAGTGAATGAAATTTCTAAA 1320  
QY 1321 AATGGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATATATGTT 1380  
DB 1321 AATGGTTATCATTAGGGCTTTTGAATTTATAAACTTTGGGTACTTATACTAAATATATGTT 1380  
QY 1381 AGTTATTTCTGCTTCCAGTCTTGTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440  
DB 1381 AGTTATTTCTGCTTCCAGTCTTGTGATATATTTGTTGATATTAAGATTTCTTGACTTATA 1440  
QY 1441 TTTTGAATGGGTTCTAGTGAAGAAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1500  
DB 1441 TTTTGAATGGGTTCTAGTGAAGAAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1500  
QY 1501 ATTTTACACTCTTGTATTTACAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGG 1560  
DB 1501 ATTTTACACTCTTGTATTTCTCAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGG 1560  
QY 1561 AAAAGTCAAGTGAACCAAAAAAAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGG 1620  
DB 1561 AAAAGTCAAGTGAACCAAAAAAAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGGAAATGAGG 1620  
QY 1621 A 1621  
DB 1621 A 1621

Search completed: December 31, 2006, 12:54:19  
Job time : 1261.98 secs

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:14:13 ; Search time 5186.18 Seconds  
(without alignments)  
6976.201 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgatttcattcatgtat.....acttgataaaggaccggt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_est7.\*  
7: gb\_est8.\*  
8: gb\_est9.\*  
9: gb\_est10.\*  
10: gb\_est11.\*  
11: gb\_est12.\*  
12: gb\_est13.\*  
13: gb\_est14.\*  
14: gb\_est15.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	427.8	66.2	478	1	AI732098
2	411.2	63.7	461	1	AA225199
3	376.6	58.3	447	1	AI732238
4	373.8	57.9	480	2	BF855163
5	373.6	57.8	447	4	EX096004
6	359.6	55.7	500	1	AA225313
7	356.4	55.2	541	11	AQ545351
8	355	55.0	456	1	AI734072
9	353.8	54.8	546	11	AQ469231
10	335.8	52.0	713	14	AG183700
11	313.6	48.5	533	12	CG891636
12	298.8	46.3	481	11	AQ199998
13	292.2	45.2	474	11	AQ171162
14	241.4	37.4	578	11	AQ726978
15	232.2	35.9	407	11	AQ598346
16	221.6	34.3	767	7	BF679787
17	216.2	33.5	698	7	BF676535
18	212.2	32.8	374	1	AA639908
19	202	31.3	578	9	DA878876

20	186	28.8	560	9	DA868489
C 21	177.2	27.4	234	1	AA579128
22	168.6	26.1	1512	2	BF965166
C 23	112.4	17.4	397	1	AA507792
24	101.4	15.7	683	2	EG924354
25	97	15.0	784	11	AQ782590
26	92.4	14.3	475	11	AQ496973
27	77.2	12.0	716	14	AG179840
C 28	66	10.2	369	2	BG998422
29	63	9.8	76	14	AG187983
C 30	54	8.4	310	7	BE142028
C 31	53.8	8.3	466	12	CE814791
32	53.8	8.3	674	12	CE482447
33	53.8	8.3	762	12	CE283656
C 34	53.4	8.3	272	7	BE168137
C 35	52.8	8.2	407	8	CV317561
C 36	51.4	8.0	343	1	AI672225
37	51.2	7.9	394	7	BF368099
C 38	50.2	7.8	861	12	BZ874654
C 39	49.8	7.7	644	14	AG038156
C 40	49	7.6	300	7	BF368114
41	47	7.3	818	14	CT386427
42	47	7.3	877	14	CT109462
43	46.8	7.2	836	9	DN287707
C 44	46.8	7.2	860	9	DN288889
45	46.4	7.2	883	12	CC576958

## ALIGNMENTS

RESULT 1  
AI732098  
LOCUS AI732098 478 bp mRNA linear EST 14-JUN-1999  
DEFINITION nc22g03.x5 NCI\_CGAP\_Prl Homo sapiens cDNA clone IMAGE:1008916, mRNA sequence.  
ACCESSION AI732098  
VERSION AI732098.1 GI:5053233  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 478)  
AUTHORS NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.llnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone  
Original clone citation: WashU-NCI EST Project  
This read has been verified (found to hit its original self in the correct orientation)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 431.

FEATURES  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1008916"  
/sex="Male"

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/dev stage="45 years old"
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/clone_lib="NCI_CGAP_Prl"
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strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

```

## ORIGIN

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Query Match      66.2%; Score 427.8; DB 1; Length 478;
Best Local Similarity 97.6%; Pred. No. 5.4e-117;
Matches 456; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

QY 137 GATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTTGTGCCACCCCTCTGACCCCT 196
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Db 69 TTGGAACTCCTGTGACCCCTTTAGAACAGCCTTACCTAATATCTGCTAGAGAAAGACCAA 128

QY 257 CAACGGCCTCAAGAGATCTTACCATGAAGTCTCAGCTAATCTTGGCTAAGATGTGG 316
Db 129 CAACGGCCTCAAGAGATCTTACCATGAAGTCTCAGCTAATCTTGGCTAAGATGTGG 188

QY 317 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCAATTTGTGTGGAT 376
Db 189 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCAATTTGTGTGGAT 248

QY 377 AAAGTCAGATGCCAGGGGCGAGAGAGGGGCTTGTCTTTGGGAACAATGGCTGAG 436
Db 249 AAAGTCAGATGCCAGGGGCGAGAGAGGGGCTTGTCTTTGGGAACAATGGCTGAG 307

QY 437 CATATAACCATAGTTATGGGGAACAAACAAACATCAAGTCACCTGTATCAATTTGCCATG 496
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QY 497 AAGACTTGAGGACCTGTAATCTACCGATTATCTTTAAGGACGAGGACGAGTTTGAAGTGG 556
Db 365 AAGACTTGAGGACCTGTAATCTACCGATTATCTTTAAGGACGAGGACGAGTTTGAAGTGG 424

QY 557 CCAACATGCAGCAGCAGATCAATGGAAACACACAGATGATGCAAT 603
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RESULT 2
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DEFINITION National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
sequence.
ACCESSION AA225199
VERSION AA225199.1 GI:1846507
KEYWORDS EST.
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Homo.
1 (bases 1 to 461)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```

```

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -41m13 fwd. EF from Amersham
High quality sequence stop: 367.
Location/Qualifiers
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/sex="Male"
/clone_lib="NCI_CGAP_Prl"
/notes="Vector: PAMP10; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

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## FEATURES

source

## ORIGIN

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Query Match      63.7%; Score 411.2; DB 1; Length 461;
Best Local Similarity 96.5%; Pred. No. 5.3e-112;
Matches 440; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

QY 137 GATCTGCTAGCAAGAGAAACAAACACTGATCTCTTTTGTGCCACCCCTCTGACCCCT 196
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QY 197 TTGGAATCTCTTGACCCCTTTAGAACAGGCTACTAATATCTGCTAGAGAAAGACCAA 256
Db 61 TTGGAATCTCTTGACCCCTTTAGAACAGGCTACTAATATCTGCTAGAGAAAGACCAA 120

QY 257 CAACGGCCTCAAGAGATCTCTTACCATGAAGGTCCTAGCTAATTTCTTGGCTAAGATGTGG 316
Db 121 CAACGGCCTCAAGAGATCTCTTACCATGAAGGTCCTAGCTAATTTCTTGGCTAAGATGTGG 180

QY 317 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCAATTTGTGTGGAT 376
Db 181 GTTCCACATAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCAATTTGTGTGGAT 240

QY 377 AAAGTCAGATGCCAGGGGCGAGAGAGGGGCTTGTCTTTGGGAACAATGGCTGAG 436
Db 241 AAAGTCAGATGCCAGGGGCGAGAGAGGGGCTTGTCTTTGGGAACAATGGCTGAG 299

QY 437 CATATAACCATAGGTTATGGGGAACAAACAAACATCAAGTCACCTGTATCAATTTGCCATG 496
Db 300 CATATAACCATAGG---TATGGGAACAAACAAACATCAAGTCACCTGTATCAATTTGCCATG 356

QY 497 AAGACTTGAGGACCTGTAATCTACCGATTATCTTTAAGGACGAGGACGAGTTTGAAGTGG 556
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QY 557 CCAACATGCAGCAGCAGATCAATGGAAACACACAGATGATGCAAT 592
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## RESULT 3

AI732238/c

LOCUS

AI732238

447 bp

mRNA

linear

EST 13-DEC-1999

nf31g01.x5 NCI\_CGAP\_Prl Homo sapiens cDNA clone IMAGE:915408  
sequence.  
similar to contains element MSRI repetitive element ;, mRNA

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AI732238.1 GI:50533351  
EST.  
Homo sapiens (human)  
Homo sapiens  
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 447)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui,  
M.D., Michael Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

This read is a RESEQUENCE of a previously sequenced human clone  
Original clone citation: National Cancer Institute, Cancer Genome  
Anatomy Project (CGAP), Tumor Gene Index  
This read has been verified (found to hit its original self in the  
correct orientation)  
Insert Length: 621 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 423.  
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strand cDNA was primed with oligo(dT)17 on 50 ng of  
DNase-treated, total cellular RNA obtained from  
5,000-10,000 microdissected, histologically normal  
prostate epithelial cells. Double-stranded cDNA was  
ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
cDNA with an adaptor-specific primer, and the resulting  
PCR product subcloned into pAMP10 by the UDG-cloning  
method (Life Technologies). Average insert size is 600  
bp. NOTE: Not directionally cloned. This library was  
constructed by David Krizman."

FEATURES  
source

Query Match 58.3%; Score 376.6; DB 1; Length 447;  
Best Local Similarity 95.7%; Pred. No. 1.4e-101;  
Matches 420; Conservative 0; Mismatches 14; Indels 5; Gaps 3;

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QY 238 CTGCTAGAGAAAGACCAACAGCGCTCAAGAGTCTCTTACCATGAAGGCTCAGCTA 297  
DB 387 CTGCTAGAGAAAGACCAACAGCGCTCAAGAGTCTCTTACCATGAAGGCTCAGCTA 328  
QY 298 ATTCTTGGGTAGAGTGGGTTCACATTAGGTTCTGAATATGGGGGAA-GGGTCAATT 356  
DB 327 ATTCTTGGGTAGAGTGGGTTCACATTAGGTTCTGAATATGGGGGAAAGGGTCAATT 268

QY 357 TGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTG 416  
DB 267 TGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTG 209  
QY 417 CTTTGGGAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACACATCAAG 476  
DB 208 CTTTGGGAACAATGGCTGAGCATATAACCATAGG---TATGGGAACAAAAACATCAAG 152  
QY 477 TCACGTGTATCAATGGCATGAAGACTTGAGGACCTGAACTTACCGATTCATCTTAAGGC 536  
DB 151 TCACGTGTATCAATGGCATGAAGACTTGAGGACCTGAACTTACCGATTCATCTTAAGGC 92  
QY 537 AGCAGGACCAAGTTGAGTGGCAACAATGCAGCAGCAGAGATCAATGGAACAAACAGAAATGA 596  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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RC3-FN0201-111100-011-f05 FN0201 Homo sapiens cDNA, mRNA sequence.  
BF855163.1 GI:12242907  
EST.  
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Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 480)  
Dias Neto,S., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC3&t2=RC3-FN0201-111100-011-f05&t3=2000-11-11&t4=1>)  
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application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

FEATURES  
source



REFERENCE 1 (bases 1 to 500)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@emil.nih.gov](mailto:cgaps@emil.nih.gov)  
M.D., Michael Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
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High quality sequence stop: 367.

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strand cDNA was primed with oligo(dT)17 on 50 ng of  
DNase-treated, total cellular RNA obtained from  
5,000-10,000 microdissected, histologically normal  
prostate epithelial cells. Double-stranded cDNA was  
ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
cDNA with an adaptor-specific primer, and the resulting  
PCR product subcloned into pAMP10 by the UDG-cloning  
method (Life Technologies). Average insert size is 600  
bp. NOTE: Not directionally cloned. This library was  
constructed by David Krizman."

ORIGIN  
Query Match 55.7%; Score 359.6; DB 1; Length 500;  
Best Local Similarity 94.8%; Pred. No. 1.8e-96;  
Matches 458; Conservative 0; Mismatches 15; Indels 10; Gaps 8;  
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DB 485 GATCTGCTAGCAAA-GAAGAAGAAACAACACATGATCTCTTCTGCGCCACCTCTGACCC 426  
QY 195 CTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACTAATATCTCTAGAGAAAAGACC 254  
DB 425 CTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACTAATATCTCTAGAGAAAAGACC 366  
QY 255 AACACGGCC-TCAAAGGATCTCTTACCATGAAGTCT-CAGCTAATCTTGGCTAAGAT 312  
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QY 313 GTGGGTTCCACATTAGGTTCTGATATGGGGGAGGCTCAATTTGCTCTATTGTGCT 372  
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ACCESSION AQ545351  
VERSION AQ545351.1 GI:4904594  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 541)  
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and  
Venter,J.C.  
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready  
Map Building  
Unpublished (1997)  
Other-GSSs: CITBI-EI-2613A22.TP  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [hbs@tigr.org](mailto:hbs@tigr.org)  
Clones are available from Research Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC  
end search page:  
[http://www.tigr.org/tdb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html).  
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Class: BAC ends.

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QY 61 TGCTCAGGGGAGGTTTCATATGGGACTTTCTACTGCCAAGGTTCTATACAGGATATAA 120  
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QY 121 GNGGCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAAACACTGATCTTTCTG 180  
DB 200 GTGGCTCACAGTATAGATCTGGTAGCAAGAAGAAAGAAACAAACACTGATCTTTCTG 259  
QY 181 CCACCCCTCTGACCTTTGGAACTCCTCTGACCCCTTTAGAACAGCTTACCTTAATCTG 240  
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/sex="male"
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/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"

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Best Local Similarity 90.6%; Pred. No. 1.1e-94;
Matches 413; Conservative 0; Mismatches 33; Indels 10; Gaps 3;

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DB 78 ATGATTTTCATTATCATGTAAATCAGATCACTCAAGGGGCCAACCAACAGCTGGAGCCAC 137
QY 61 TGCCTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
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QY 121 GGGCCCTCACAGTATAGATCTGTAGCAAGAAGAACAAACAACTGATCTTTCTG 180
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QY 181 CACCCCTCTGACCTTTGGAATCTCTCTGACCTTTAGAACAGCTCACTAATATCTG 240
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QY 241 CTAGAGAAAGACCAACAGGCTCAAGAGTCTCTTACCATCAAGGCTCTCAGCTAAT 300
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DB 488 GGGAACTGGCTCAGCATATACCATAGTTATGG 523

RESULT 10
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LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-057E05.TU, genomic survey
sequence.
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AG183700
VERSION
AG183700.1 GI:16713380
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE
1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
2 (bases 1 to 713)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

COMMENT
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. 713
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-057E05.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

FEATURES
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ORIGIN
Query Match 52.0%; Score 335.8; DB 14; Length 713;
Best Local Similarity 82.1%; Pred. No. 3e-89;
Matches 463; Conservative 0; Mismatches 83; Indels 18; Gaps 6;

QY 1 ACGATTTTCATTATCATGTAAATCGGTCTACTCAAGGGGCCAACCAACAGCTGGAGCCAC 60
DB 137 ACAATTTTCATTATCATGTAAATCAATCACTCAAGGGGCCAACCAACAGCTGGAGCCAC 196
QY 61 TGCCTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB 197 TGCTCAGGCAAGGTTTCATATGGGACTTTTATCTGCCCAACGCTCTATACAGGATATAA 256
QY 121 GGGCCCTCACAGTATAGATCTGTAGCAAGAAGAACAAACAACTGATCTTTCTG 180
DB 257 GGTGCTCCTCACTGATACAGATCTGGAGCA---AAGAGAAACAAACAACTGATCTTTCTG 313
QY 181 CACCCCTCTGACCTTTGGAATCTCTGACCTTTAGAACAGCTCACTAATATCTG 240
DB 314 CCAC-----ATTATTTGAACCCCTCTCAGCTTTAGAACAGCCCACTAATCTG 365
QY 241 CTAGAGAAAGACCAACAGGCTCAAGAGTCTCTTACCATCAAGGCTCTCAGCTAAT 300
DB 366 CAGCGAAAGACCAACA---GTTTCAAGAGTCTCTTACCATCAAGGCTCTCAGTAAAT 422
QY 301 CTGGCTAAGATGTGGTTCCACATAGGTT-CTGAATATGGGGGAAGGCTCAATTTGCT 359
DB 423 ACTTGTAGATGTGGTTCCACATAGGTTCTTCTGAATATGTGGGAAGGCTCAATTTCTC 482
QY 360 TCATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGTTGCTT 419
DB 483 TCACCTTTGTGTGGATAAAGTCAGATGCTCAGCGCCATAGTAGGGGACTGTGCTT 542
QY 420 TGGGACATGCTGAGCATATAACCATAGTATATGGGAACAAACACATCAAGTCA 479
DB 543 TGGGAACAATGTTGGCCCTTATACGTATAGGT--ATGGCAACTAAAAACATGACAGCCA 600
QY 480 C-TGATCAATTTGCCATGAAGACTTTGAGGAGCTGAATCTACCGATTTCACTTAAGGCGAG 538
DB 601 CTTGTATCAATCGTCATGAAGACTTTGAGGAGCTGAATCTACTGCAATTTTAAAGGCAC 660
QY 539 CAGGACCACTTTGAGTGGCAACA 562
DB 661 CAGGACCACTTTGAGTGGCAACA 684

RESULT 11
CG891636
LOCUS
DEFINITION
Ygm24306 Yunnan snub-nosed monkey genomic BAC library Pygathrix
bieti genomic clone 24306, genomic survey sequence.
CG891636
LOCUS
DEFINITION
Ygm24306 Yunnan snub-nosed monkey genomic BAC library Pygathrix
bieti genomic clone 24306, genomic survey sequence.
CG891636
LOCUS
DEFINITION
Ygm24306 Yunnan snub-nosed monkey genomic BAC library Pygathrix
bieti genomic clone 24306, genomic survey sequence.
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ACCESSION CG891636  
 VERSION CG891636.1 GI:51792549  
 KEYWORDS GSS.  
 SOURCE Pygathrix bieti (black snub-nosed monkey)  
 ORGANISM Pygathrix bieti  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Cercopithecoidea; Colobinae; Pygathrix.  
 1 (bases 1 to 533)  
 Xu, H.L., Qian, Y.P., Yang, F.T., Nie, W.H., Chi, J.X. and Su, B.  
 Construction and characterization of bacterial artificial  
 chromosome (BAC) library of Yunnan snub-nosed monkey (*Rhinopithecus*  
*biei*)  
 Unpublished (2003)  
 Contact: Xu, H.L.; Su, B.  
 Key Laboratory of Cellular and Molecular Evolution  
 Kunming Institute of Zoology, the Chinese Academy of Sciences  
 32 Jiaochangdonglu, Kunming, Yunnan 650223, People's Republic of  
 China  
 Email: xuhl@mail.kiz.ac.cn  
 Seq primer: 17  
 Class: BAC ends.  
 JOURNAL Location/Qualifiers  
 COMMENT 1. 533  
 /organism="Pygathrix bieti"  
 /mol\_type="genomic DNA"  
 /strain="Yunnan snub-nosed monkey"  
 /db\_xref="taxon:61621"  
 /clone="24306"  
 /sex="male"  
 /tissue\_type="Skin"  
 /cell\_type="Fibroblast"  
 /cell\_line="KCB96009"  
 /clone\_lib="Yunnan snub-nosed monkey BAC library"  
 /note="Vector: pBACe3.6; Site 1: EcoRI; Genomic DNA was  
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 Recombinants were transformed into DH10B."  
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 Location/Qualifiers  
 1. 533  
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 /db\_xref="taxon:9606"  
 /clone="RPCI-11-61C21"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /clone\_lib="RPCI-11"  
 /note="vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 RPCI11 Human Male BAC Library"  
 ORIGIN  
 Query Match 48.5%; Score 313.6; DB 12; Length 533;  
 Best Local Similarity 83.8%; Pred. No. 1.3e-82;  
 Matches 394; Conservative 0; Mismatches 61; Indels 15; Gaps 3;  
 QY 68 GGAAGGTTTCATATGGGACTTTCTACTGCCAGGTTCTATACAGGATATAAGNGCCT 127  
 Db 12 GGAAGGTTTCATATGGGACTTTCTACTGCCAGGTTCTATACAGGATATAAGTACT 71  
 QY 128 CACAGTATAGTCTGTAGCAAGAGAGAAACAAACACATGATCTCTTTCTGCCACCCC 187  
 Db 72 CACAGTACAGATCTGTAGCAAGAGAGAGAAACAAACGCTGATCTCTTTCTGCCA 127  
 QY 188 TCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCTACCTAATATCTGCTAGAGA 247  
 Db 128 ---TTTATTGTAACCCCTCTGACCCCTTTAGAACAGTGCAATTAATATCTGCTAAGA 183  
 QY 248 AAAGACCAACACGGCTCAAGGATCTTTACCATGAAGTCTCAGCTAATCTTGCT 307  
 Db 184 AAAGACCAACCAAGGCTCAAGGATCTCGTACCATGAAGTCTCAGCTAATCTTGCT 243  
 QY 308 AAGATGTGGTTCCACATTTAGGTCTGTAATATGGGGGAAGGTCATTTGCTCAATTTG 367  
 Db 244 AAGATGCGGTTTCCACATTTAGGTCTGTAATATGGGGGAAGGTCATTTGCTCAATTTG 303  
 QY 368 TGTGTGGATAAAGTCCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTTGGGAACA 427  
 Db 304 TGTGTGGATAAAGGAGGATGCTCAGCGCCAGAGCAGGGTCTG-GTGCTTTGGGAACA 362  
 QY 428 ATGGCTGAGCATATAACCATAGGTTATGG-----GGAAACAACAACATCAAGTCACT 481  
 Db 363 ATGACTGAGCAATAAGCATAGGAATGGGAACATACAAACATTTGAACCTCAAGCCACT 422  
 QY 482 GTATCAATTGGCATGAAGACTTGAGGACCTCAATCTACCGATTTCATCTT 531

Db 423 GTATGACTTGCCATGAAGACTTGAGGACTCTGAATCAGTAAGGCGCATCTT 472  
 RESULT 12  
 LOCUS AQ199998  
 DEFINITION RPCI11-61C21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-61C21,  
 genomic survey sequence.  
 ACCSSON AQ199998 481 bp DNA linear GSS 20-APR-1999  
 VERSION AQ199998.1 GI:3612197  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 481)  
 Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,  
 Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.  
 Use of human BAC End Sequences for Sequence-Ready Map Building  
 Unpublished (1998)  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdadams@tigr.org  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html  
 Class: BAC ends.  
 Location/Qualifiers  
 1. 481  
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 /db\_xref="taxon:9606"  
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 /sex="Male"  
 /cell\_type="Lymphocytes"  
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 RPCI11 Human Male BAC Library"  
 ORIGIN  
 Query Match 46.3%; Score 298.8; DB 11; Length 481;  
 Best Local Similarity 89.6%; Pred. No. 3.6e-78;  
 Matches 346; Conservative 0; Mismatches 29; Indels 11; Gaps 2;  
 QY 4 ATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCACTGC 63  
 Db 107 ATTTTCATTATCATGTAAATCACATCACTCAAGGGGCCAACACACAGCTGGAGCCACTGC 166  
 QY 64 TCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGTTCATACAGGATATAAGGN 123  
 Db 167 TCAGGGGAAGTTTCATACGGGACTTTCTACTGCCCAAGTTCATACAGGATATAAGGT 226  
 QY 124 GCCTCACAGTATACATCTGTAGCAAGAGAGAAACAAACACACTGATCTCTTTCTGCCA 183  
 Db 227 GCCTCACAGTATACATCTGTAGCA---AGAGGAACACAGACTGACCTCTCTCTGCCA 283  
 QY 184 CCCCTCTGACCCCTTTGGAACCTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTGCTA 243  
 Db 284 C-----ATTATTGAACCCCTCTCACCCCTTTAGAACAGCCCTACCTAATCTGCCA 335  
 QY 244 GAGAAAAAGACCAACACGGCCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATCTTT 303  
 Db 336 GAGAAAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATCTCT 395

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QY 304 GGCTAAGATGTGGTTCACATTAAGTTCCTGAATATGGGGGAGGCTCAATTGCTCAT 363
Db 396 GGCTAAGATGTGGTTCACATTAAGTTCCTGAATATGGGGGAGGCTCAATTGCTCAC 455
QY 364 TTGTGTGTGGATAAAGTCAGGATGC 389
Db 456 TCTGTGTGGGATAAAGTCAGGATGC 481

RESULT 13
LOCUS AQ1711162 474 bp DNA linear GSS 17-OCT-1998
DEFINITION HS 3070_B1_B09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=17 Row=D, genomic survey sequence.
ACCESSION AQ1711162.1 GI:3568529
VERSION GSS.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 474)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kelller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3070 row: D column: 17
Class: BAC ends
High quality sequence stop: 474.
Location/Qualifiers
1..474
/organism="Homo sapiens"
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/clone="Plate=3070 Col=17 Row=D"
/sex="male"
/clone.lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3070 Col=17 Row=D"
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/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

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Query Match 45.2%; Score 292.2; DB 11; Length 474;
Best Local Similarity 89.9%; Pred. No. 3.5e-76;
Matches 338; Conservative 0; Mismatches 29; Indels 9; Gaps 2;

QY 1 ACAGATTTTCATTATCATGTAAATCGGCTCACTCAAGGGGCCAACACAGCTGGAGCCAC 60
Db 107 ATGATTTTCATTATCATGTAAATCAGATCACTCAAGGGGCCAACACAGCTGGAGCCAC 166
QY 61 TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGATATAA 120
Db 167 TGTCT-TGGGGAAGGCTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGATATAA 225
QY 121 GGGGCTCTCAGTATAGTCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 180
Db 226 GGTGGCTCTACTGTGTAGATCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 285
QY 181 CCACCCCTCTGACCCCTTGGAACCTCTCTGACCCCTTTAGAACAAAGGCTACCTAATATCTG 240
Db 286 CCAC-----ATTATTTGAACCCCTCTGACCCCTTTATAACAAGCCCTCATATCTG 337

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QY 241 CTAGAGAAAAGCAACCAACGGCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
Db 338 CTAGAGAAAAGCAACCAACGGCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 397
QY 301 CTTGGCTAAGATGTGGTTCACATTAAGTTCCTGAATATGGGGGAGGCTCAATTGCT 360
Db 398 CTTAGCTAAGATGTGGTTCACATTAAGTTCCTGAATATGGGGGAGGCTCAATTGCT 457
QY 361 CATTGTTGTGTGGAT 376
Db 458 CACTTGTGTGCGGAT 473

RESULT 14
LOCUS AQ726978 578 bp DNA linear GSS 14-JUL-1999
DEFINITION HS_5416_B2_F06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=992 Col=12 Row=L, genomic survey sequence.
ACCESSION AQ726978
VERSION GSS.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 578)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kelller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 992 row: L column: 12
Seq primer: T7
Class: BAC ends
High quality sequence stop: 578.
Location/Qualifiers
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/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

FEATURES
source
1..578
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=992 Col=12 Row=L"
/sex="male"
/clone.lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 37.4%; Score 241.4; DB 11; Length 578;
Best Local Similarity 82.6%; Pred. No. 7.3e-61;
Matches 314; Conservative 0; Mismatches 57; Indels 9; Gaps 3;

QY 1 ACAGATTTTCATTATCATGTAAATCGGCTCACTCAAGGGGCCAACACAGCTGGAGCCAC 60

```

Db 166 ACGATTTCATATCATGTGATCAGATCATCTCAAGGGGCCAACACCAACTGGGAGCCAC 225  
 Qy 61 TGCTCAGGGGAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120  
 Db 226 TGAT-AGGGGAGGCTCATATGGGACTATCTACTGCTTAAAGTTCAACACAGGAAATAAA 284  
 Qy 121 GGNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAGAACCAACACTGATCTCTTCTG 180  
 Db 285 GGCGCCTCAGTGTGTAAACTGGTAGCAAAACAAACACCGATCTCTATCCG 344  
 Qy 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG 240  
 Db 345 CCAC-----ATTATTAGACACCCCTCTGACCCCTTTATACAGCCCAACCCCATATCTG 397  
 Qy 241 CTAGAGAAAAGACCAACACCGCCTCAAGGATCTCTTACCATGAAGTCTCTCAGCTAATT 300  
 Db 398 CTAGAAAAAGACCAACACCGCCTGTAAGGATCTCTTACCATGAAGTCTCTCAACTAATT 457  
 Qy 301 CTGGCTAAGATGTGGGTTCCACATTAGGTTCTGNAATATGGGGGAAGGTTCAATTGCG- 359  
 Db 458 CTTAACTAAGATGTGGGGTTCAATTATGTTCTCGAAAACAGAGAGAGGGTTCATATTGCG 517  
 Qy 360 TCATTTTGTGTGGATAAA 379  
 Db 518 TCACTTTGTGTGATAGA 537

RESULT 15  
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 LOCUS  
 DEFINITION HS\_5233\_B2\_G02\_SP6E RPCI-11 Human Male BAC Library Homo sapiens  
 genomic clone Plates=809 Col=4 Row=N, genomic survey sequence.  
 ACCESSION A0598346  
 VERSION A0598346.1 GI:5029558  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 407)  
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 10449764  
 Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
 or from Research Genetics (<http://info@resgen.com>). BAC end Web Server:  
<http://www.htsc.washington.edu>  
 Plate: 809 row: N column: 4  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 407.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=809 Col=4 Row=N"  
 /sex="male"  
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FEATURES  
 source

/note="vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACE3.6 vector at EcoRI sites"

## ORIGIN

Query Match 35.9%; Score 232.2; DB 11; Length 407;  
 Best Local Similarity 86.2%; Pred. No. 3.8e-58;  
 Matches 294; Conservative 0; Mismatches 35; Indels 12; Gaps 3;  
 Qy 4 ATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGAGCCACTGC 63  
 Db 77 ATTTTCATTATCATGTAAATCAATCACTCAAGGGGCCAACACAGCTGGGAGCCACTGC 136  
 Qy 64 TCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCAACAGGTTCTATACAGGATATAAGGN 123  
 Db 137 TCATGGCAAGGTTTCATACGGGACTTTCTACTGCCAACAGGTTCTATACAGGATATAAGGT 196  
 Qy 124 GCCTCACAGTATAGATCTGGTAGCAAGAGAGAGAAACAAACACTGATCTCTTTCTGCCA 183  
 Db 197 GCCTCACAGTACAGATCTGGTTTCA--AAGAGAGAAACAGACACTGACCTCTCTTCTGCCA 253  
 Qy 184 CCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACTAATATCTGCTA 243  
 Db 254 C-----ATTATATGAACCCCTCTCACCCTTTATACAGGCCCACTAATCTGCCA 305  
 Qy 244 GAGAAAAGACCAACACAGGCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAATTTCT 303  
 Db 306 GAGAAAAGACCAACACAGGCTCATAGGATCTCTTACCATGAAGGTTCTCAGCTAATTTCT 365  
 Qy 304 GGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGG 344  
 Db 366 GGCTAAGATGTGGGTT-CACATTAGGTTCTGAATTTGGGGTG 405

Search completed: December 31, 2006, 19:30:44  
 Job time : 5191.18 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:22:01 ; Search time 1030.23 seconds  
(without alignments)  
7716.790 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgattttcattcatgtgta.....acttgataaaaggagccgt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	100.0	647	3	US-09-759-143-308 Sequence 308, App
2	646	100.0	647	3	US-09-780-669-308 Sequence 308, App
3	646	100.0	647	3	US-09-822-827-308 Sequence 308, App
4	646	100.0	647	3	US-09-232-880-308 Sequence 308, App
5	646	100.0	647	3	US-09-895-793-308 Sequence 308, App
6	646	100.0	647	3	US-09-895-814-308 Sequence 308, App
7	646	100.0	647	6	US-10-012-896-308 Sequence 308, App
8	646	100.0	647	6	US-10-010-940-308 Sequence 308, App
9	646	100.0	647	7	US-10-144-678A-308 Sequence 308, App
10	646	100.0	647	7	US-10-294-025-308 Sequence 308, App
11	646	100.0	647	16	US-11-234-786-308 Sequence 308, App
12	600.8	93.0	2577	7	US-10-294-025-1034 Sequence 1034, App
13	599.2	92.8	1481	9	US-10-357-930-21476 Sequence 21476, A
14	599.2	92.8	1481	9	US-10-357-930-21536 Sequence 21536, A
15	599.2	92.8	1481	9	US-10-357-930-21562 Sequence 21562, A
16	599.2	92.8	1481	9	US-10-357-930-21578 Sequence 21578, A
17	599.2	92.8	1481	9	US-10-357-930-22089 Sequence 22089, A

C 18	599.2	92.8	1481	9	US-10-357-930-25779	Sequence 25779, A
C 19	599.2	92.8	1481	9	US-10-357-930-27378	Sequence 27378, A
C 20	599.2	92.8	1481	9	US-10-357-930-27404	Sequence 27404, A
C 21	599.2	92.8	1481	9	US-10-357-930-27951	Sequence 27951, A
22	599.2	92.8	2577	3	US-09-759-143-552	Sequence 552, App
23	599.2	92.8	2577	3	US-09-780-669-552	Sequence 552, App
24	599.2	92.8	2577	3	US-09-822-827-552	Sequence 552, App
25	599.2	92.8	2577	3	US-09-895-793-552	Sequence 552, App
26	599.2	92.8	2577	3	US-09-895-814-552	Sequence 552, App
27	599.2	92.8	2577	6	US-10-012-896-552	Sequence 552, App
28	599.2	92.8	2577	7	US-10-144-678A-552	Sequence 552, App
29	599.2	92.8	2577	7	US-10-294-025-552	Sequence 552, App
30	599.2	92.8	2577	16	US-11-234-786-552	Sequence 552, App
31	597.6	92.5	1454	3	US-09-957-708-14	Sequence 14, Appl
32	597.6	92.5	1454	16	US-11-230-251-14	Sequence 14, Appl
C 33	463.6	71.8	974	12	US-10-301-480-547960	Sequence 547960
C 34	463.6	71.8	974	12	US-10-301-480-1161369	Sequence 1161369
C 35	460.4	71.3	974	12	US-10-301-480-587040	Sequence 587040
C 36	460.4	71.3	974	12	US-10-301-480-1200449	Sequence 1200449
37	459.8	71.2	603	4	US-09-925-065A-893115	Sequence 893115
38	459.8	71.2	603	5	US-09-925-065A-893115	Sequence 893115
C 39	447.2	69.2	1065	4	US-09-925-065A-721218	Sequence 721218
C 40	447.2	69.2	1065	5	US-09-925-065A-721218	Sequence 721218
41	434.2	67.2	668	4	US-09-925-065A-489987	Sequence 489987
42	434.2	67.2	668	5	US-09-925-065A-489987	Sequence 489987
C 43	408.2	63.2	554	12	US-10-301-480-241350	Sequence 241350
C 44	408.2	63.2	554	12	US-10-301-480-241351	Sequence 241351
C 45	408.2	63.2	554	12	US-10-301-480-241352	Sequence 241352

#### ALIGNMENTS

#### RESULT 1

US-09-759-143-308

; Sequence 308, Application US/09759143

; Patent No. US2002002248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John H.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 308

; LENGTH: 647

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(647)

; OTHER INFORMATION: n = A,T,C or G

; US-09-759-143-308

Query Match 100.0%; Score 646; DB 3; Length 647;





;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
;; FILE REFERENCE: 210121.534C1  
;; CURRENT APPLICATION NUMBER: US/09/822,827  
;; CURRENT FILING DATE: 2001-03-28  
;; NUMBER OF SEQ ID NOS: 982  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 308  
;; LENGTH: 647  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(647)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-822-827-308

Query Match 100.0%; Score 646; DB 3; Length 647;  
Best Local Similarity 100.0%; Pred. No. 2.7e-201;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60  
DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60  
QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120  
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120  
QY 121 GNGGCTCAGATATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTTTCTG 180  
DB 121 GNGGCTCAGATATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTTTCTG 180  
QY 181 CCACCCCTCGACCTTCGAACTCTGAACTCTGACCCCTTTAGAACAAAGCTACCTAAATATCG 240  
DB 181 CCACCCCTCGACCTTCGAACTCTGAACTCTGACCCCTTTAGAACAAAGCTACCTAAATATCG 240  
QY 241 CTAGAGAAAAGACCAACACGGCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300  
DB 241 CTAGAGAAAAGACCAACACGGCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300  
QY 301 CTTGGCTAAGATGTGGGTTCCATTAAGTTCTGAAATATGGGGGAAGGTTCAATTTGCT 360  
DB 301 CTTGGCTAAGATGTGGGTTCCATTAAGTTCTGAAATATGGGGGAAGGTTCAATTTGCT 360  
QY 361 CATTTTGTGTGGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420  
DB 361 CATTTTGTGTGGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420  
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAAGTCAAC 480  
DB 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAAGTCAAC 480  
QY 481 TGTATCAATTGGCATGAAGACTTGAGGGACCTGAATCTACCGATTCACTTAAGGCAGCA 540  
DB 481 TGTATCAATTGGCATGAAGACTTGAGGGACCTGAATCTACCGATTCACTTAAGGCAGCA 540  
QY 541 GGACCAAGTTTGAGTGGCAACATGCAGCAGAGATCAATGGAACACAGATGATGTC 600  
DB 541 GGACCAAGTTTGAGTGGCAACATGCAGCAGAGATCAATGGAACACAGATGATGTC 600  
QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATAAAGGGGACCGT 647  
DB 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATAAAGGGGACCGT 647

## RESULT 4

US-09-232-880-308  
; Sequence 308, Application US/09232880  
; Publication No. US20020182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn

;; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
;; FILE REFERENCE: 210121.428C6  
;; CURRENT APPLICATION NUMBER: US/09/232,880  
;; CURRENT FILING DATE: 1999-01-15  
;; NUMBER OF SEQ ID NOS: 338  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 308  
;; LENGTH: 647  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(647)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-232-880-308

Query Match 100.0%; Score 646; DB 3; Length 647;  
Best Local Similarity 100.0%; Pred. No. 2.7e-201;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60  
DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACACAGCTGGAGCCAC 60  
QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120  
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120  
QY 121 GNGGCTCAGATATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTTTCTG 180  
DB 121 GNGGCTCAGATATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTTTCTG 180  
QY 181 CCACCCCTCGACCTTCGAACTCTGAACTCTGACCCCTTTAGAACAAAGCTACCTAAATATCG 240  
DB 181 CCACCCCTCGACCTTCGAACTCTGAACTCTGACCCCTTTAGAACAAAGCTACCTAAATATCG 240  
QY 241 CTAGAGAAAAGACCAACACGGCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300  
DB 241 CTAGAGAAAAGACCAACACGGCTCAAGAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300  
QY 301 CTTGGCTAAGATGTGGGTTCCATTAAGTTCTGAAATATGGGGGAAGGTTCAATTTGCT 360  
DB 301 CTTGGCTAAGATGTGGGTTCCATTAAGTTCTGAAATATGGGGGAAGGTTCAATTTGCT 360  
QY 361 CATTTTGTGTGGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420  
DB 361 CATTTTGTGTGGATAAGTCAAGATGCCCAGGGGCCAGACGAGGGGCTGCTGCTTT 420  
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAAGTCAAC 480  
DB 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACACATCAAAGTCAAC 480  
QY 481 TGTATCAATTGGCATGAAGACTTGAGGGACCTGAATCTACCGATTCACTTAAGGCAGCA 540  
DB 481 TGTATCAATTGGCATGAAGACTTGAGGGACCTGAATCTACCGATTCACTTAAGGCAGCA 540  
QY 541 GGACCAAGTTTGAGTGGCAACATGCAGCAGAGATCAATGGAACACAGATGATGTC 600  
DB 541 GGACCAAGTTTGAGTGGCAACATGCAGCAGAGATCAATGGAACACAGATGATGTC 600  
QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATAAAGGGGACCGT 647  
DB 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATAAAGGGGACCGT 647

## RESULT 5

US-09-895-793-308  
; Sequence 308, Application US/09895793  
; Publication No. US20020192763A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.

```
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGGATCTCTTACCATGAAGGTCTCAGCTAATTT 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGGATCTCTTACCATGAAGGTCTCAGCTAATTT 180
Qy 181 CCACCCCTTGACCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTTGACCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
Qy 241 CTAGAGAAAGACCAACACGGCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATTT 300
Db 241 CTAGAGAAAGACCAACACGGCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATTT 300
Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Db 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360
Qy 361 CATTTTGTGTGGTAAGTACAGATGCCAGGGGCCAGACAGCGGCTCTGCTTT 420
Db 361 CATTTTGTGTGGTAAGTACAGATGCCAGGGGCCAGACAGCGGCTCTGCTTT 420
Qy 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGAAACAAAACATCAAAAGTCTAC 480
Db 421 GGGAAACAATGGCTGAGCATATACCATAGGTTATGGGAAACAAAACATCAAAAGTCTAC 480

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-814-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGGATCTCTTACCATGAAGGTCTCAGCTAATTT 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGGATCTCTTACCATGAAGGTCTCAGCTAATTT 180
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QY 181 CCACCCCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG 240
Db 181 CCACCCCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTTACCATGAAGGCTCAGCTAAT 300
Db 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTTACCATGAAGGCTCAGCTAAT 300
QY 301 CTTGGCTTAAGATCTGGTTCCACATTAAGTTCTGAAATATGCGGGGGAAGGCTCAATTTGCT 360
Db 301 CTTGGCTTAAGATCTGGTTCCACATTAAGTTCTGAAATATGCGGGGGAAGGCTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTGCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGGAACAAACAACATCAAGTCCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGGAACAAACAACATCAAGTCCAC 480
QY 481 TGTATCAATGGCCATGAAGACTTGGGGACCTCAATCTTACCGATTCTTAAAGGCAGCA 540
Db 481 TGTATCAATGGCCATGAAGACTTGGGGACCTCAATCTTACCGATTCTTAAAGGCAGCA 540
QY 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAAACAACAGATGATTCG 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAAACAACAGATGATTCG 600
QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATATAAAGGGGACCGT 647
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## RESULT 7

US-10-012-896-308  
; Sequence 308, Application US/10012896  
; Publication No. US20020183251A1

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skelky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Wantanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C27  
; CURRENT APPLICATION NUMBER: US/10/012,896  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 1011  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 308  
; LENGTH: 647  
; TYPE: DNA  
; ORGANISM: Homo sapiens

; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 123  
; OTHER INFORMATION: n = A,T,C or G  
US-10-012-896-308

Query Match 100.0%; Score 646; DB 6; Length 647;  
Best Local Similarity 100.0%; Pred. No. 2.7e-201;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ACATTTTTCATTTATCATGTAAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
Db 1 ACATTTTTCATTTATCATGTAAATCGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60
QY 61 TCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
Db 61 TCCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
QY 121 GNGCCTCACAGTATAGATCTGGTAGCAAAAGAGAAAGAAACAAACACATGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAAAGAGAAAGAAACAAACACATGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAAACAAGCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAAACAAGCTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
Db 241 CTAGAGAAAGACCAACCAAGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
QY 301 CTTGGCTAAGATGTGGGTTTCCACATTAAGTTCTGAAATATGGGGGAAGGCTCAATTTGCT 360
Db 301 CTTGGCTAAGATGTGGGTTTCCACATTAAGTTCTGAAATATGGGGGAAGGCTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTGCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAAACAATAGTTTATGGGGAACAAACAACATCAAGTCCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAAACAATAGTTTATGGGGAACAAACAACATCAAGTCCAC 480
QY 481 TGTATCAATTTGCCATGAAGACTTTAGGGACCTGAATCTACCGATTCTTAAAGGCAGCA 540
Db 481 TGTATCAATTTGCCATGAAGACTTTAGGGACCTGAATCTACCGATTCTTAAAGGCAGCA 540
QY 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAAACAACAGATGATTCG 600
Db 541 GGACCAAGTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAAACAACAGATGATTCG 600
QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGTATATAAAGGGGACCGT 647
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## RESULT 8

US-10-010-940-308  
; Sequence 308, Application US/10010940  
; Publication No. US2003008062A1

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqiu  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Stolk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

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; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1) --(647)
; OTHER INFORMATION: n = A,T,C or G
US-10-010-940-308

Query Match      100.0%; Score 646; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180

Qy 181 CCACCCCTTGACCTTTGGAACTCTCTGACCTTTTGAACAAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTTGACCTTTGGAACTCTCTGACCTTTTGAACAAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAAT 300
Db 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAAT 300

Qy 301 CTGTGCTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360
Db 301 CTGTGCTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360

Qy 361 CATTTTGTGTGGATTAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATTAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420

Qy 421 GGGACAAATGGCTGAGCATATAACCATAGTTTATGGGAACAAACAAACATCAAAAGTCAC 480
Db 421 GGGACAAATGGCTGAGCATATAACCATAGTTTATGGGAACAAACAAACATCAAAAGTCAC 480

Qy 481 TGTATCAATTTGCCATGAAGACTTTGAGGACCTTGAATCTACCGATTTCATCTTAAAGCAGCA 540
Db 481 TGTATCAATTTGCCATGAAGACTTTGAGGACCTTGAATCTACCGATTTCATCTTAAAGCAGCA 540

Qy 541 GGACAGTTTGTAGTGGCAACAATCAGCAGCAGAGATCAATGAAACAAACAGATGATTCG 600
Db 541 GGACAGTTTGTAGTGGCAACAATCAGCAGCAGAGATCAATGAAACAAACAGATGATTCG 600

Qy 601 AATGTCCTTTTTTTTCTCTGCTCTCTGACTTATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTCTCTGACTTATAAAGGGGACCGT 647
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## RESULT 9

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US-10-144-678A-308
; Sequence 308, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

```
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-10-144-678A-308
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Query Match      100.0%; Score 646; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTTCTG 180

Qy 181 CCACCCCTTGACCTTTGGAACTCTCTGACCTTTTGAACAAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTTGACCTTTGGAACTCTCTGACCTTTTGAACAAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAAT 300
Db 241 CTAGAGAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAAT 300

Qy 301 CTGTGCTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360
Db 301 CTGTGCTAAGATGTGGTTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCT 360

Qy 361 CATTTTGTGTGGATTAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATTAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420

Qy 421 GGGACAAATGGCTGAGCATATAACCATAGTTTATGGGAACAAACAAACATCAAAAGTCAC 480
Db 421 GGGACAAATGGCTGAGCATATAACCATAGTTTATGGGAACAAACAAACATCAAAAGTCAC 480
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; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21536
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 4
; OTHER INFORMATION: n = A, T, C or G
; US-10-357-930-21476

Query Match      92.8%; Score 599.2; DB 9; Length 1481;
Best Local Similarity 98.0%; Pred. No. 1.1e-185;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

QY 1 ACGATTTTCATTATCATGTAAATCGGTCATCGGTCACCTCAAGGGGCCACACAGCTGGAGCCAC 60
DB 1097 ACGATTTTCATTATCATGTAAATCGGTCATCGGTCACCTCAAGGGGCCACACAGCTGGAGCCAC 1038

QY 61 TGGTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGAGTCTTATACAGGATATAA 120
DB 1037 TGGTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGAGTCTTATACAGGATATAA 978

QY 121 GGGCCCTCAGATATAGATCTGGTAGCAAGAAGAAAGAAACAACTGATCTCTTTCTG 180
DB 977 GGTGCCTCAGATATAGATCTGGTAGCAAGAAGAAAGAAACAACTGATCTCTTTCTG 918

QY 181 CCACCCCTCTGACCTTTGGAATCTCTGACCCCTTAGAACAGGCTTACCTAATATCTG 240
DB 917 CCACCCCTCTGACCTTTGGAATCTCTGACCCCTTAGAACAGGCTTACCTAATATCTG 858

QY 241 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGCTCTCAGCTAAT 300
DB 857 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGCTCTCAGCTAAT 798

QY 301 CTTGGCTTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGCTCAATTTGCT 360
DB 797 CTTGGCTTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGCTCAATTTGCT 738

QY 361 CATTTTGTGTGGATAAAGTCAAGATGCCAGGGGCCAGAGCAGGGGCTGCTCTTTT 420
DB 737 CATTTTGTGTGGATAAAGTCAAGATGCCAGGGGCCAGAGCAGGGGCTGCTCTTTT 679

QY 421 GGGACAATGGCTGAGCATATTAACATAGTTTATGGGGAACAAAACAACTCAAGTCTAC 480
DB 678 GGGACAATGGCTGAGCATATTAACATAGTTTATGGGGAACAAAACAACTCAAGTCTAC 622

QY 481 TGTATCAATTGGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 540
DB 621 TGTATCAATTGGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 562

QY 541 GGACCAAGTTTGTAGTGGCAACAATGCAAGCAGAGAGATCAATGGAACAAACAGATGATTC 600
DB 561 GGACCAAGTTTGTAGTGGCAACAATGCAAGCAGAGAGATCAATGGAACAAACAGATGATTC 502

QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGTATAAAGG 641
DB 501 AATGTCCTTTTCTCTGCTTCTGACTTGTATAAAGG 461
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## RESULT 14

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US-10-357-930-21536/c
; Sequence 21536, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
```

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; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21536
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 4
; OTHER INFORMATION: n = A, T, C or G
; US-10-357-930-21536
```

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Query Match      92.8%; Score 599.2; DB 9; Length 1481;
Best Local Similarity 98.0%; Pred. No. 1.1e-185;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

QY 1 ACGATTTTCATTATCATGTAAATCGGTCATCGGTCACCTCAAGGGGCCACACAGCTGGAGCCAC 60
DB 1097 ACGATTTTCATTATCATGTAAATCGGTCATCGGTCACCTCAAGGGGCCACACAGCTGGAGCCAC 1038
```

```
QY 61 TGGTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGAGTCTTATACAGGATATAA 120
DB 1037 TGGTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGAGTCTTATACAGGATATAA 978

QY 121 GGGCCCTCAGATATAGATCTGGTAGCAAGAAGAAAGAAACAACTGATCTCTTTCTG 180
DB 977 GGTGCCTCAGATATAGATCTGGTAGCAAGAAGAAAGAAACAACTGATCTCTTTCTG 918

QY 181 CCACCCCTCTGACCTTTGGAATCTCTGACCCCTTAGAACAGGCTTACCTAATATCTG 240
DB 917 CCACCCCTCTGACCTTTGGAATCTCTGACCCCTTAGAACAGGCTTACCTAATATCTG 858

QY 241 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGCTCTCAGCTAAT 300
DB 857 CTAGAGAAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGCTCTCAGCTAAT 798

QY 301 CTTGGCTTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGCTCAATTTGCT 360
DB 797 CTTGGCTTAAGATGTGGGTTCCACATTAAGTTCTGAATATGGGGGAAGGCTCAATTTGCT 738

QY 361 CATTTTGTGTGGATAAAGTCAAGATGCCAGGGGCCAGAGCAGGGGCTGCTCTTTT 420
DB 737 CATTTTGTGTGGATAAAGTCAAGATGCCAGGGGCCAGAGCAGGGGCTGCTCTTTT 679

QY 421 GGGACAATGGCTGAGCATATTAACATAGTTTATGGGGAACAAAACAACTCAAGTCTAC 480
DB 678 GGGACAATGGCTGAGCATATTAACATAGTTTATGGGGAACAAAACAACTCAAGTCTAC 622

QY 481 TGTATCAATTGGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 540
DB 621 TGTATCAATTGGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTCATCTTAAGGAGCA 562

QY 541 GGACCAAGTTTGTAGTGGCAACAATGCAAGCAGAGAGATCAATGGAACAAACAGATGATTC 600
DB 561 GGACCAAGTTTGTAGTGGCAACAATGCAAGCAGAGAGATCAATGGAACAAACAGATGATTC 502
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Qy 601 AATGCTCTTTTCTCCTCTGCTGACTTGATAAAGGG 641  
Db ||||||||||||||||||||||||||||||||||||||||  
501 AATGCTCTTTTCTCCTCTGCTGACTTGATAAAGGG 461  
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RESULT 15

US-10-357-930-21562/c  
; Sequence 21562, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Endege, Wilson  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 62232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21562  
; LENGTH: 1481  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..2..3..4  
; OTHER INFORMATION: n = A,T,C or G  
US-10-357-930-21562

Query Match 92.8%; Score 599.2; DB 9; Length 1481;  
Best Local Similarity 98.0%; Pred. No. 1.1e-185;  
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 60  
Db ||||||||||||||||||||||||||||||||||||||||  
1097 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 1038  
Qy 61 TGCTCAGGGGAGGTTTCATATGGGACTTCTACTCCCAAGGTTCTATACAGGATATAA 120  
Db ||||||||||||||||||||||||||||||||||||||||  
1037 TGCTCAGGGGAGGTTTCATATGGGACTTCTACTCCCAAGGTTCTATACAGGATATAA 978  
Qy 121 GGGGCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACTGATCTCTTTCTG 180  
Db ||||||||||||||||||||||||||||||||||||||||  
977 GGTGCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACTGATCTCTTTCTG 918  
Qy 181 CCACCCCTCTGACCTTTGGAACTCCTCTGACCCCTTTAGAACAAAGCTACCTAATATCTG 240  
Db ||||||||||||||||||||||||||||||||||||||||  
917 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAAAGCTACCTAATATCTG 858  
Qy 241 CTAGAGAAAGAACCAACAGCCCTCAAGAGATCTTTACCATGAAGTCTCAGCTAATT 300  
Db ||||||||||||||||||||||||||||||||||||||||  
857 CTAGAGAAAGAACCAACAGCCCTCAAGAGATCTTTACCATGAAGTCTCAGCTAATT 798  
Qy 301 CTTGGCTAAGATGTGGGTTCACATTAGGTTCTGAATATGGGGGAAAGGTCATTTGCT 360  
Db ||||||||||||||||||||||||||||||||||||||||  
797 CTTGGCTAAGATGTGGGTTCACATTAGGTTCTGAATATGGGGGAAAGGTCATTTGCT 738

Qy 361 CATTTCGTGTGTGATAAAGTCAGGATGCCAGGGCCAGAGAGGGGCTGCTTGTCTTT 420  
Db ||||||||||||||||||||||||||||||||||||||||  
737 CATTTCGTGTGTGATAAAGTCAGGATGCCAGGGCCAGAGAGGGGCTGCTGCTTT 679  
Qy 421 GGGAAACAATGGCTGAGCATATAAACCATAGGTTATGGGGAAACAAACATCAAAGTCAC 480  
Db ||||||||||||||||||||||||||||||||||||||||  
678 GGGAAACAATGGCTGAGCATATAAACCATAGG---TATGGGAACAAACAAACATCAAAGTCAC 622  
Qy 481 TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540  
Db ||||||||||||||||||||||||||||||||||||||||  
621 TGTATCAATTGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 562  
Qy 541 GGACCACTTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAAACAGATGATTGC 600  
Db ||||||||||||||||||||||||||||||||||||||||  
561 GGACCACTTTGAGTGGCAACAATGCAGCAGCAGCAATCAATGGAACAAACAGATGATTGC 502  
Qy 601 AATGTCCTTTTCTCTCTGCTTCTGACTTTGATAAAGGG 641  
Db ||||||||||||||||||||||||||||||||||||||||  
501 AATGTCCTTTTCTCTCTGCTTCTGACTTTGATAAAGGG 461

Search completed: December 31, 2006, 13:56:01  
Job time : 1032.23 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:26:03 ; Search time 222.451 Seconds  
(without alignments)  
6266.684 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgatttcattcatgtgta.....acttgataaaagggaacggt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3050214 seqs, 1077301958 residues

Total number of hits satisfying chosen parameters: 6100428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	100.0	647	US-11-344-932-308	Sequence 308, App
2	599.2	92.8	2577	US-11-344-932-552	Sequence 552, App
3	58.6	9.1	201	US-10-284-444-1570	Sequence 1570, App
4	36.6	5.7	1566	US-11-174-307B-221	Sequence 221, App
5	36.6	5.7	1566	US-11-056-355B-75529	Sequence 75529, A
6	36	5.6	1145	US-10-953-349-1766	Sequence 1766, App
7	35.4	5.5	715	US-11-266-748A-407591	Sequence 407591, App
8	35.4	5.5	715	US-11-266-748A-478637	Sequence 478637, App
9	34.8	5.4	74930	US-11-454-296-1	Sequence 1, Appli
10	34.6	5.4	943	US-11-266-748A-214211	Sequence 214211, App
11	34.6	5.4	945	US-11-266-748A-76796	Sequence 76796, A
12	34.6	5.4	945	US-11-266-748A-129607	Sequence 129607, App
13	34.4	5.3	87977	US-11-330-726-145	Sequence 145, App
14	33.8	5.2	2704	US-11-056-355B-46304	Sequence 46304, A
15	33.4	5.2	633	US-11-454-296-35	Sequence 35, Appl
16	33.4	5.2	142281	US-11-266-748A-23957	Sequence 23957, A
17	33	5.1	572	US-11-266-748A-215548	Sequence 215548, App
18	32.6	5.0	1472	US-10-449-902-19300	Sequence 19300, A
19	32.6	5.0	1472	US-10-449-902-19357	Sequence 19357, A
20	32.6	5.0	3538	US-10-449-902-25041	Sequence 25041, A
21	32.4	5.0	1308	US-11-293-582-14	Sequence 14, Appl
22	32.4	5.0	119057	US-10-539-228-609	Sequence 609, App

23	32.4	5.0	254396	6	US-10-540-898-534	Sequence 534, App
24	32.4	5.0	816609	10	US-11-073-360-1606	Sequence 1606, App
25	32.4	5.0	663	7	US-11-371-354-10070	Sequence 10070, A
26	32.2	5.0	663	7	US-11-371-354-75580	Sequence 75580, A
27	32.2	5.0	2907	6	US-10-612-783-1529	Sequence 1529, App
28	32.2	5.0	3031	9	US-11-218-305-1072	Sequence 1072, App
29	32.2	5.0	189056	8	US-11-266-748A-100812	Sequence 100812, A
30	32	5.0	521	8	US-11-266-748A-153623	Sequence 153623, App
31	32	5.0	521	8	US-11-338-399-9	Sequence 9, Appli
32	32	5.0	1611	8	US-11-174-307B-2477	Sequence 2477, App
33	32	5.0	1855	9	US-11-056-355B-101312	Sequence 101312, App
34	32	5.0	1855	9	US-11-056-355B-112551	Sequence 112551, App
35	32	5.0	1855	9	US-11-174-307B-321	Sequence 321, App
36	32	5.0	1856	9	US-11-056-355B-37911	Sequence 37911, A
37	32	5.0	3021	6	US-10-449-902-25119	Sequence 25119, A
38	32	5.0	3667	6	US-10-449-902-23178	Sequence 23178, A
39	32	5.0	794	8	US-11-266-748A-39970	Sequence 39970, A
40	31.6	4.9	794	8	US-11-266-748A-214583	Sequence 214583, App
41	31.6	4.9	794	8	US-11-266-748A-237140	Sequence 237140, App
42	31.6	4.9	3883	6	US-10-449-902-18938	Sequence 18938, A
43	31.6	4.9	73634	10	US-11-330-726-121	Sequence 121, App
44	31.6	4.9	811284	6	US-10-833-833-128	Sequence 128, App
45	31.6	4.9	811284	6	US-10-833-833-128	Sequence 128, App

#### ALIGNMENTS

#### RESULT 1

US-11-344-932-308  
; Sequence 308, Application US/11344932  
; Publication No. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitchem, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Deng, Ta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C32  
; CURRENT APPLICATION NUMBER: US/11/344,932  
; CURRENT FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: 10/144,678  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 10/012,896  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 09/895,814  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/852,911  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: 09/780,669  
; PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-308

Query Match      100.0%; Score 646; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 9.9e-205; Mismatches 0; Indels 0; Gaps 0;
Matches 647; Conservative 0;

Qy 1 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACACAGCTGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACACAGCTGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GGGGCTCACAGTATAGATCTGGTAGCAAGAGAGAGAAACAAACACATGATCTCTTCTG 180
Db 121 GGGGCTCACAGTATAGATCTGGTAGCAAGAGAGAGAAACAAACACATGATCTCTTCTG 180

Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACACCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACACCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAAGCAACCAACCGCCTCAAGAGATCTCTTACATGAAGGTCTCAGCTAATT 300
Db 241 CTAGAGAAAAGCAACCAACCGCCTCAAGAGATCTCTTACATGAAGGTCTCAGCTAATT 300

Qy 301 CTTGGCTAAGATGTGGTTCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTAAGATGTGGTTCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Qy 361 CATTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420
Db 361 CATTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT 420

Qy 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAAACATCAAAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAAACATCAAAAGTCAC 480

Qy 481 TGTATCAATGCGCATGAAGACTTGGGACCTGAATCTACCGATTCATCTTAAAGCAGCA 540
Db 481 TGTATCAATGCGCATGAAGACTTGGGACCTGAATCTACCGATTCATCTTAAAGCAGCA 540

Qy 541 GGACCAAGTTTGAAGTGGCAACAAATGACGAGCAGAGATCAATGGAACAAACAGAAATGTC 600
Db 541 GGACCAAGTTTGAAGTGGCAACAAATGACGAGCAGAGATCAATGGAACAAACAGAAATGTC 600

Qy 601 AATGTCCTTTTCTCTCTGCTTCTGACTTGAATAAAAGGGACCGT 647
Db 601 AATGTCCTTTTCTCTCTGCTTCTGACTTGAATAAAAGGGACCGT 647
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RESULT 2

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US-11-344-932-552
; Sequence 552, Application US/11344932
; Publication No. US20060269532A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 552
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-552

Query Match      92.8%; Score 599.2; DB 7; Length 2577;
Best Local Similarity 98.0%; Pred. No. 8.8e-189;
Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

Qy 1 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 60
Db 636 ACGATTTTCATTATCATGTAATCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 695

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
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;; PRIOR FILING DATE: 2004-02-13  
;; NUMBER OF SEQ ID NOS: 119966  
;; SEQ ID NO 75529  
;; LENGTH: 1566  
;; TYPE: DNA  
;; ORGANISM: Arabidopsis thaliana  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(1566)  
;; OTHER INFORMATION: Ceres Seq. ID no. 6443376  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(1566)  
;; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 15175923  
;; OTHER INFORMATION: as cited in SEQ ID NO 54037  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(1566)  
;; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13503610  
;; OTHER INFORMATION: as cited in SEQ ID NO 62416  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(1566)  
;; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13657610  
;; OTHER INFORMATION: as cited in SEQ ID NO 66165  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(1566)  
;; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13598312  
;; OTHER INFORMATION: as cited in SEQ ID NO 68448  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(1566)  
;; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13596100  
;; OTHER INFORMATION: as cited in SEQ ID NO 68573  
US-11-056-355B-75529  
  
Query Match 5.7%; Score 36.6; DB 9; Length 1566;  
Best Local Similarity 53.1%; Pred. No. 0.31;  
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
  
QY 371 GTGGATAAAGTCAGGATGCCAGGGCCAGAGCAGGGGGCTGCTTGGGAACAATG 430  
Db 1372 GAGGCTAAGTAGGATGAAGAAACCGGGTTGGCAGATGCTTTGGAAAGTGGG 1431  
  
QY 431 GCTGAGCATATAACCATAGGTTATGGGGAACAAACATCAAAAGTCACCTGTATCAATT 490  
Db 1432 TTTAAGTGTAACAGTGCAGTTTGGGTGGCTCTTAAACAATGTCAAGCCCTTCGGTTAGTATC 1491  
  
QY 491 GCCATGAAGACTTGAGGGACCTGAATC 517  
Db 1492 COTGGGAACACTGCATCGACCGATATC 1518  
  
RESULT 6  
US-10-953-349-1766/c  
;; Sequence 1766, Application US/10953349  
;; Publication No. US20060107345A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ALEXANDROV, Nickolai et al.  
;; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
;; FILE REFERENCE: 2750-1579PUS2  
;; CURRENT APPLICATION NUMBER: US/10/953,349  
;; CURRENT FILING DATE: 2004-09-30  
;; NUMBER OF SEQ ID NOS: 40252  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 1766  
;; LENGTH: 1145  
;; TYPE: DNA  
;; ORGANISM: Arabidopsis thaliana  
US-10-953-349-1766

Query Match 5.6%; Score 36; DB 6; Length 1145;  
Best Local Similarity 48.5%; Pred. No. 0.41;  
Matches 99; Conservative 0; Mismatches 105; Indels 0; Gaps 0;  
  
QY 400 GAGCAGGGGCTGCTTGGGAACAATGGCTGAGCATATTAACCATAGTTATGGGA 459  
Db 900 GACCAAGAGGCCACATATGAGAATCACAGCGTATAAGCTAAATCCATAAGAAGTGCATC 841  
  
QY 460 ACAAACAACATCAAGTCACTGTATCAATTCCTCAAGACTTGAGGGACCTGAATCTA 519  
Db 840 CATTTATCTTACCACATCATCACCGTCTCCNAAGCGTTGCCCTACTTGGTCCCAATACCCGTG 781  
  
QY 520 CCGATTTCATCTTAAGGCAGCAGGACCACTTGTAGTGGCAACAATGCAGCAGCAATCAA 579  
Db 780 CCGCTCGTACCCTCCCTGAGCCGAGGAAGAGTCTCCACGATGACTCAGCAGAACAG 721  
  
QY 580 TGGAAACAACAGAAATGATTGCAAT 603  
Db 720 TCCAAGCACAATTTGTGGCATCAGT 697  
  
RESULT 7  
US-11-266-748A-407591/c  
;; Sequence 407591, Application US/11266748A  
;; Publication No. US20060134663A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Hartkin, Paul  
;; APPLICANT: Johnston, Patrick  
;; APPLICANT: Mulligan, Karl  
;; TITLE OF INVENTION: Transcriptome Microarray Technology and  
;; TITLE OF INVENTION: Methods of Using the Same  
;; FILE REFERENCE: 55815-0102 (319189)  
;; CURRENT APPLICATION NUMBER: US/11/266,748A  
;; CURRENT FILING DATE: 2005-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105479.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105482.6  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105483.4  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105507.0  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105485.9  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105484.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: US 60/662,276  
;; PRIOR FILING DATE: 2005-03-14  
;; PRIOR APPLICATION NUMBER: US 60/700,293  
;; PRIOR FILING DATE: 2005-07-18  
;; NUMBER OF SEQ ID NOS: 483996  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 407591  
;; LENGTH: 715  
;; TYPE: DNA  
;; ORGANISM: Homo Sapiens  
US-11-266-748A-407591  
  
Query Match 5.5%; Score 35.4; DB 8; Length 715;  
Best Local Similarity 66.2%; Pred. No. 0.5;  
Matches 51; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
  
QY 28 TCATCTAAGGGGCCAACACACAGCTGGGAGCCACTGCTCAGGGGAGGTTTCATATGGGACT 87  
Db 317 TGATTCCAGTGGGAGCCAGGTTTGGGAACCACTTCTATGGGAGTGCTCATCTGGGAAT 258  
  
QY 88 TTCTACTGCCCAAGGTT 104  
Db 257 TGGCTGTCCACAGGGTT 241  
  
RESULT 8  
US-11-266-748A-478637

; Sequence 478637, Application US/11266748A  
; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700,293

; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: Patentin version 3.3

; SEQ ID NO 478637

; LENGTH: 715

; TYPE: DNA

; ORGANISM: Homo Sapiens

; US-11-266-748A-478637

Query Match 5.5%; Score 35.4; DB 8; Length 715;

Best Local Similarity 66.2%; Pred. No. 0.5;

Matches 51; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 28 TCACCTACGGGGCAACACAGCTGGGAGCCATGTCAGGGGAAGTTTCATATGGGACT 87

DB 399 TGATCCAGTGGGCGCCAGCTTGGGAACCACTTCTATGGGGATGGTCCATCTGGGAAT 458

QY 88 TTCTACTGCCCAAGGTT 104

DB 459 TGGCTGTCCACAGGTT 475

RESULT 9

US-11-454-296-1/c

; Sequence 1, Application US/11454296

; Publication No. US2006028658A1

; GENERAL INFORMATION:

; APPLICANT: GRANT, Struan F. A.

; APPLICANT: SAINZ, Jesus

; TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR

; TITLE OF INVENTION: RISK OF TYPE 2 DIABETES MELLITUS

; FILE REFERENCE: 2345.2069-002

; CURRENT APPLICATION NUMBER: US/11/454,296

; CURRENT FILING DATE: 2006-06-16

; PRIOR APPLICATION NUMBER: US 60/692,174

; PRIOR FILING DATE: 2005-06-20

; PRIOR APPLICATION NUMBER: US 60/757,155

; PRIOR FILING DATE: 2006-01-06

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: Patentin version 3.3

; SEQ ID NO 1

; LENGTH: 74930

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-11-454-296-1

Query Match 5.4%; Score 34.8; DB 7; Length 74930;

Best Local Similarity 51.7%; Pred. No. 1.1;  
Matches 78; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 12 TATCATGTAATCGGTCTACTCAAGGGCCCAACCCAGCTGGGAGCCACTGCTTCAGGGGA 71

DB 50371 TAACATTAAGACAGTTTCTACTCAGGAACCAACAGAACTTAGACAACTGCTTTAGAAGC 50312

QY 72 AGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTTCTATACAGGATATAAAGGNGSCCTCACA 131

DB 50311 ACATGGAGAGAGCCCTTATGCTTCTCAAGGCCAACTCTACTTAATCCATCAGTTAATGAAT 50252

QY 132 GTATAGATCTGTAGCAAAAGAAAGAAACA 162

DB 50251 GCTTGGAGGGGATATAAGATATAAGGAGACA 50221

RESULT 10

US-11-266-748A-214211/c

; Sequence 214211, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700,293

; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: Patentin version 3.3

; SEQ ID NO 214211

; LENGTH: 943

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (869)..(869)

; OTHER INFORMATION: n is a, c, g, or t

; US-11-266-748A-214211

Query Match 5.4%; Score 34.6; DB 8; Length 943;

Best Local Similarity 53.3%; Pred. No. 1.1;

Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 347 AGGGTCAATTTGCTCATTTTGTGTGGATAAAGTCAGGATCCAGGGGGCCAGACAGG 406

DB 657 AGGGTAATAAAGTGGGCTTCTTAGGTCGCAAGAAATTCGGGTCTACTCGGGCTACTTTCCG 598

QY 407 GGGCTGCTTGTGGGAACAATGGCTGAGCATATAACCATAGGTTATGGGAACAAAAC 466

DB 597 GAATTCCTTTAGTGTGGGCTTTAGGGCACTGCACTCTCACACCAGCTGATGGGAACCATCTG 538

QY 467 AACATCAAAAGTCACTGT 483

DB 537 GATACCTGACTCACTGT 521

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RESULT 11
US-11-266-748A-76796/c
; Sequence 76796, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76796
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-76796

Query Match      5.4%; Score 34.6; DB 8; Length 945;
Best Local Similarity 53.3%; Pred. No. 1.1;
Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 347 AGGTCATTTGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGCCAGAGCAGG 406
Db 683 AGGGTAAAGTGGGCTTCTTAGTCTGCAAGAAATTCGGGTTGTACTCGGGCTACTTTCCG 624
QY 407 GGGCTGCTTGTCTTGGGAACAATGCTGAGCATATAACCATAGGTTATGGGGAACAAAC 466
Db 623 GAATTCCTTAGTGGGCTTAGGGCACTGCATCTCACACGCTGATGGGAACCATCTG 564
QY 467 AACATCAAAGTCACTGT 483
Db 563 GATACCTGACTCACTGT 547

RESULT 12
US-11-266-748A-129607
; Sequence 129607, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
```

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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129607
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-129607

Query Match      5.4%; Score 34.6; DB 8; Length 945;
Best Local Similarity 53.3%; Pred. No. 1.1;
Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 347 AGGTCATTTGCTCATTTTGTGTGGATAAAGTCAGGATGCCAGGGCCAGAGCAGG 406
Db 263 AGGGTAAAGTGGGCTTCTTAGTCTGCAAGAAATTCGGGTTGTACTCGGGCTACTTTCCG 322
QY 407 GGGCTGCTTGTCTTGGGAACAATGCTGAGCATATAACCATAGGTTATGGGGAACAAAC 466
Db 323 GAATTCCTTAGTGGGCTTAGGGCACTGCATCTCACACGCTGATGGGAACCATCTG 382
QY 467 AACATCAAAGTCACTGT 483
Db 383 GATACCTGACTCACTGT 399

RESULT 13
US-11-330-726-145
; Sequence 145, Application US/11330726
; Publication No. US20060204982A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 20366-011002
; CURRENT APPLICATION NUMBER: US/11/330,726
; CURRENT FILING DATE: 2006-01-12
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 87977
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (2001)..(2048)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (6720)..(7498)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (8834)..(8882)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: misc.feature
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LOCATION: (16167)..(16186)  
OTHER INFORMATION: n = a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (24443)..(24580)  
OTHER INFORMATION: n = a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (28778)..(28871)  
OTHER INFORMATION: n = a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (45952)..(46750)  
OTHER INFORMATION: n = a, c, g, or t  
US-11-330-726-145

Query Match 5.3%; Score 34.4; DB 10; Length 87977;  
Best Local Similarity 53.8%; Pred. No. 16;  
Matches 71; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 316 GGTTCACATAGTCTCAATATGGGGGAGGGTCAATTTGCTCATTTTGTGTGGA 375.  
DB 70644 GCTGTCCCATGATGCTCTGACTATAACAGTACTGTGTCAGGGGCAAACTGGGAGCA 70703

QY 376 TAAAGTCAGGATGCCCGAGGGCCAGACGAGGGGGCTGTGTTTGGGAACAATGGCTGA 435  
DB 70704 TCATCTCATTTGGAATCACAGAGAAAGCAGGGGTATGCTCCCAATGGGAGCAGAGCTGA 70763

QY 436 GCATATAACCAT 447  
DB 70764 GCACATAAAGAT 70775

RESULT 14  
US-11-056-355B-46304/c  
Sequence 46304, Application US/11056355B  
Publication No. US20060150283A1  
GENERAL INFORMATION:  
APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nikolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
TITLE OF INVENTION: Polypeptides Encoded Thereby  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,190  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 46304  
LENGTH: 2704  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2704)  
OTHER INFORMATION: Ceres Seq. ID no. 13578529  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2704)  
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13582297  
OTHER INFORMATION: as cited in SEQ ID NO 56486  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2704)  
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13586936  
OTHER INFORMATION: as cited in SEQ ID NO 0  
US-11-056-355B-46304

Query Match 5.2%; Score 33.8; DB 9; Length 2704;  
Best Local Similarity 52.5%; Pred. No. 3.6;  
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 463 AAACACATCAAGTCACTGTATCAATTGCCATGAGACTTGAGGACCTGAATCTACCG 522

DB 753 ACACAAACAAGAACATCAACAGGACGATTTCATGAGCATCAGGGATATTAGGATCTGCTC 694  
QY 523 ATTCACTTTAAGGACGAGGACCACTTTGAGTGGCAACAATGCCAGCAGCAATCAATGG 582  
DB 693 CTACACTCAAAAGCAACTTGAACAATCCAAAGGAATTCACAGAAGCACCAGAAGCAGCGC 634  
QY 583 AAACAACAGAAATGATTGCAAT 603  
DB 633 AATGAAGACGACTACTTTTAT 613

RESULT 15  
US-11-454-296-35/c  
Sequence 35, Application US/11454296  
Publication No. US20060286588A1  
GENERAL INFORMATION:  
APPLICANT: GRANT, Struan P. A.  
APPLICANT: SAINZ, Jesus  
TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR  
TITLE OF INVENTION: RISK OF TYPE 2 DIABETES MELLITUS  
FILE REFERENCE: 2345.2069-002  
CURRENT APPLICATION NUMBER: US/11/454,296  
CURRENT FILING DATE: 2006-06-16  
PRIOR APPLICATION NUMBER: US 60/692,174  
PRIOR FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: US 60/757,155  
PRIOR FILING DATE: 2006-01-06  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 35  
LENGTH: 633  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-454-296-35

Query Match 5.2%; Score 33.4; DB 7; Length 633;  
Best Local Similarity 60.4%; Pred. No. 2.2;  
Matches 55; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 12 TATCATGTAAATCGGGTCACTCAAGGGGCCAACACAGCTGGGAGCCACTGCTCAGGGGA 71  
DB 141 TAACATTAAAGACAGTTTCACTCAGGAAACCAACAGAACTTAGACACAATGCTTAGAAGC 82  
QY 72 AGGTTCAATCGGACTTTCTACTGCCCAAGG 102  
DB 81 ACATGGAGACGAGCCTTTATGCTTCTCAAGG 51

Search completed: December 31, 2006, 19:49:07  
Job time : 225.451 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: December 31, 2006; 12:07:59 ; Search time 502.906 Seconds  
(without alignments)  
8969.963 Million cell updates/sec  
Title: US-09-232-880-308  
Perfect score: 646  
Sequence: 1 acgatttcattcatgtga.....acttgataaaaggagaccgt 647  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 5244920 seqs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	100.0	647	3	Aaa06540 Human imm
2	646	100.0	647	4	Aah33656 Human pro
3	646	100.0	647	4	Aah33656 Human pro
4	646	100.0	647	4	Aah02721 Prostate
5	646	100.0	647	4	Aah84970 Human pro
6	646	100.0	647	4	Aaf86940 Human P71
7	646	100.0	647	5	Acc95557 Prostate
8	646	100.0	647	6	Acc95557 Prostate
9	646	100.0	647	8	Acc95284 Prostate
10	646	100.0	647	10	Adb13758 Human pro
11	646	100.0	647	10	Adg26174 Human pro
12	646	100.0	647	15	Aef66455 Human pro
13	600.8	93.0	2577	10	Adb14484 Human pro
14	599.2	92.8	1481	5	Abv21571 Human pro
15	599.2	92.8	1481	5	Abv21485 Human pro
16	599.2	92.8	1481	5	Abv27938 Human pro
17	599.2	92.8	1481	5	Abv21587 Human pro
18	599.2	92.8	1481	5	Abv21545 Human pro

C 19	599.2	92.8	1481	5	ABV27364 Human pro
C 20	599.2	92.8	1481	5	ABV27390 Human pro
C 21	599.2	92.8	1481	5	ABV22098 Human pro
C 22	599.2	92.8	1481	5	ABV25790 Human pro
C 23	599.2	92.8	2577	4	Aah33830 Human pro
24	599.2	92.8	2577	4	Aah33830 Human pro
25	599.2	92.8	2577	5	Aas63923 Human pro
26	599.2	92.8	2577	6	AbL95294 Human P71
27	599.2	92.8	2577	8	Acc95458 Prostate
28	599.2	92.8	2577	10	Adb14002 Human pro
29	599.2	92.8	2577	10	Adg26418 Human pro
30	599.2	92.8	2577	15	Aef66699 Human pro
31	597.6	92.5	1454	6	Aad38826 Human PSN
32	401.6	62.2	452	14	ACL55651 Human col
33	357.6	55.4	815	5	ABV11648 Human pro
34	265.8	41.1	790	5	ABV11499 Human pro
35	260	40.2	671	5	ABV41718 Human pro
36	260	40.2	671	5	ABV41569 Human pro
37	260	40.2	671	5	ABV38602 Human pro
38	256.4	39.7	608	5	ABV27406 Human pro
C 39	256.4	39.7	608	5	ABV27303 Human pro
C 40	256.4	39.7	608	5	ABV25591 Human pro
41	250	38.7	616	5	ABV32793 Human pro
42	229	35.4	554	14	ACL55144 Human col
43	217.4	33.7	690	5	ABV02479 Human pro
44	214.6	33.2	543	5	ABV08703 Human pro
45	199	30.8	294	3	Aaz95017 Prostate

ALIGNMENTS

RESULT 1  
Aaa06540  
ID Aaa06540 standard; cDNA; 647 BP.

AC Aaa06540;

DT 13-JUN-2000 (first entry)

XX Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:308.

XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

XX Immunogenic; cytostatic; vaccine; ss.

XX Homo sapiens.

XX WO200004149-A2.

XX 27-JAN-2000.

XX 14-JUL-1999; 99WO-US015838.

XX 14-JUL-1998; 98US-00115453.

XX 14-JUL-1998; 98US-00116134.

XX 23-SEP-1998; 98US-00159812.

XX 23-SEP-1998; 98US-00159822.

XX 15-JAN-1999; 99US-00232149.

XX 15-JAN-1999; 99US-00232880.

XX 09-APR-1999; 99US-00288946.

XX (CORI-) CORIXA CORP.

XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

XX WPI; 2000-171268/15.

XX New polypeptide useful for treating and diagnosing prostate cancer

XX comprises an immunogenic portion of prostate tumor protein.

XX Claim 1; Page 198; 263pp; English.

XX The present invention describes isolated polypeptides, comprising an



QY 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTTT 420  
Db |||||  
QY 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTTT 420  
Db |||||  
QY 421 GGGAAACAATGGCTGAGCATATACCATAGTTATGGGGAACAAACACATCAAGTCAC 480  
Db |||||  
QY 421 GGGAAACAATGGCTGAGCATATACCATAGTTATGGGGAACAAACACATCAAGTCAC 480  
Db |||||  
QY 481 TGTATCAATTTGGCATGAAGACTTTGAGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540  
Db |||||  
QY 481 TGTATCAATTTGGCATGAAGACTTTGAGGACCTGAATCTACCGATTTCATCTTAAGGCAGCA 540  
Db |||||  
QY 541 GGACCAAGTTTGTAGTGGCAACAATGCGAGCAGAGCAATCAATGGAAACAACAGATGATTGC 600  
Db |||||  
QY 541 GGACCAAGTTTGTAGTGGCAACAATGCGAGCAGAGCAATCAATGGAAACAACAGATGATTGC 600  
Db |||||  
QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGATGATAAAGGGGACCGT 647  
Db |||||  
QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGATGATAAAGGGGACCGT 647  
Db |||||

## RESULT 3

AAS63749

ID AAS63749 standard; cDNA; 647 BP.

XX

AC AAS63749;

XX

DT 29-JAN-2002 (first entry)

XX

DE Human prostate cDNA sequence #301.

XX

KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX

OS Homo sapiens.

XX

PN WO200173032-A2.

XX

PD 04-OCT-2001.

XX

PF 27-MAR-2001; 2001WO-US009919.

XX

PR 27-MAR-2000; 2000US-00536857.

XX

PR 09-MAY-2000; 2000US-00568100.

XX

PR 12-MAY-2000; 2000US-00570737.

XX

PR 13-JUN-2000; 2000US-00593793.

XX

PR 27-JUN-2000; 2000US-00605783.

XX

PR 09-AUG-2000; 2000US-00636215.

XX

PR 29-AUG-2000; 2000US-00651236.

XX

PR 06-SEP-2000; 2000US-00657279.

XX

PR 02-OCT-2000; 2000US-00679426.

XX

PR 10-OCT-2000; 2000US-00685166.

XX

PR 09-NOV-2000; 2000US-00709729.

XX

XX (CORI-) CORIXA CORP.

XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Rector MW, Stolk JA, Day CH, Vedwick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX

XX WPI; 2001-639232/73.

XX

PT New human prostate-specific polypeptides and polynucleotides useful for

PT the diagnosis and treatment of cancer, especially prostate cancer.

XX

XX Claim 1; Page 326; 579pp; English.

XX

CC The invention relates to isolated prostate-specific polynucleotides,

CC polypeptides, fusion proteins of the polypeptides, antibodies raised

CC against the polypeptides (or antigenic epitopes derived from them) and

CC antigen-presenting cells expressing the polypeptides. The antibodies are

CC useful for detecting the presence of cancer, especially prostate cancer.

CC The polypeptides, polynucleotides and the antigen-presenting cells are

CC useful for stimulating and/or expanding T cells specific for a tumour

CC protein, and for inhibiting the development of cancer especially prostate  
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are  
CC useful for stimulating an immune response, and for treating cancer. The  
CC oligonucleotide is useful for detecting cancer. The present sequence is a  
CC prostate specific polynucleotide of the invention

XX  
SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

Query Match 100.0%; Score 646; DB 4; Length 647;

Best Local Similarity 100.0%; Pred. No. 6.6e-200;

Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACAGCTGGAGCCAC 60

Db |||||

QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCCAACACAGCTGGAGCCAC 60

Db |||||

QY 61 TGTCTAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAGGTTCTATACAGGATATAA 120

Db |||||

QY 61 TGTCTAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAGGTTCTATACAGGATATAA 120

Db |||||

QY 121 GGNCGCTCACAGTATAGATCTGTAGCAAGAGAAAGAAACAAACACTGATCTCTTCTG 180

Db |||||

QY 121 GGNCGCTCACAGTATAGATCTGTAGCAAGAGAGAAAGAAACAAACACTGATCTCTTCTG 180

Db |||||

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCTACCTAATATCTG 240

Db |||||

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCTACCTAATATCTG 240

Db |||||

QY 241 CTAGAGAAAAGACCAACACGGCCCTCAAGAGATCTCTTACCATGAAGGTCCTCAGCTAAT 300

Db |||||

QY 241 CTAGAGAAAAGACCAACACGGCCCTCAAGAGATCTCTTACCATGAAGGTCCTCAGCTAAT 300

Db |||||

QY 301 CTTGCTTAAGATGTGGTTCCACATTTAGTTCTGAATATGGGGGAAGGTCATTTGCT 360

Db |||||

QY 301 CTTGCTTAAGATGTGGTTCCACATTTAGTTCTGAATATGGGGGAAGGTCATTTGCT 360

Db |||||

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420

Db |||||

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420

Db |||||

QY 421 GGGAAACAATGGCTGAGCATATATAACATAGTTATGGGGAACAAACACATCAAGTCAC 480

Db |||||

QY 421 GGGAAACAATGGCTGAGCATATATAACATAGTTATGGGGAACAAACACATCAAGTCAC 480

Db |||||

QY 481 TGTATCAATTTGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTTCATCTTAAGCAGCA 540

Db |||||

QY 481 TGTATCAATTTGCCATGAAGACTTTGAGGGACCTGAATCTACCGATTTCATCTTAAGCAGCA 540

Db |||||

QY 541 GGACCAAGTTTGTAGTGGCAACAATGCGAGCAGAGATCAATGGAAACAACAGATGATTGC 600

Db |||||

QY 541 GGACCAAGTTTGTAGTGGCAACAATGCGAGCAGAGATCAATGGAAACAACAGATGATTGC 600

Db |||||

QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGATGATAAAGGGGACCGT 647

Db |||||

QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGATGATAAAGGGGACCGT 647

Db |||||

## RESULT 4

AAH02721

ID AAH02721 standard; cDNA; 647 BP.

XX

AC AAH02721;

XX

DT 14-JUN-2001 (first entry)

XX

DE Prostate tumour antigen determined cDNA sequence for P712P.

XX

KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;

KW prostate cancer; immunogenic; cytostatic; vaccine; ss.

XX

OS Homo sapiens.

XX

XX WO200125272-A2.

PN

```
XX 12-APR-2001.
PD
XX
XX
XX 04-OCT-2000; 2000WO-US027464.
PF
XX
XX 04-OCT-1999; 99US-0157455P.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Skeiky YAW, Reed SG, Cheever MA;
PI
XX WPI; 2001-245062/25.
DR
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
PT
XX
XX Claim 4; Page 210; 276pp; English.
PS
XX
XX The present invention describes an isolated polypeptide (I) comprising at
CC least an immunogenic portion of a prostate tumour antigen protein or its
CC variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I) prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a polynucleotide
CC that encodes a prostate specific protein are useful for detecting the
CC presence or absence of a cancer or monitoring the progression the
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
CC AAH74798 to AAH74821 and AAH74830 are sequences used in the
CC exemplification of the present invention
XX
XX Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
SQ
Query Match 100.0%; Score 646; DB 4; Length 647;
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
QY 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180
DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCCCTACCTAATATCTG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAAAGCCCTACCTAATATCTG 240
QY 241 CTAGAGAAAGAACCAACAGCCCTCAAGAGATCTCTTACCATGAAGGTCTCAGCTAAT 300
DB 241 CTAGAGAAAGAACCAACAGCCCTCAAGAGATCTCTTACCATGAAGGTCTCAGCTAAT 300
QY 301 CTTGGCTAAGATGCGGTTCCACATTAGTCTCTGAATATGGGGGAAGGTCATTTGCT 360
DB 301 CTTGGCTAAGATGCGGTTCCACATTAGTCTCTGAATATGGGGGAAGGTCATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGTCTT 420
DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGTCTT 420
QY 421 GGGAAACAATGGCTGAGCATATTAACATAGGTTATGGGGAACAAACACATCAAGTCTAC 480
DB 421 GGGAAACAATGGCTGAGCATATTAACATAGGTTATGGGGAACAAACACATCAAGTCTAC 480
QY 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAATCTACCGATTCATCTTAAGGACGA 540
DB 481 TGTATCAATTGCGATGAAGACTTTGAGGACCTGAATCTACCGATTCATCTTAAGGACGA 540
```

```
QY 541 GGACCAGTTTTCAGTGGCAACAATGCAGCAGAGATCAATGGAACCAACAGATGATTGC 600
DB 541 GGACCAGTTTTCAGTGGCAACAATGCAGCAGAGATCAATGGAACCAACAGATGATTGC 600
QY 601 AATGTCCTCTTTTTCCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
DB 601 AATGTCCTCTTTTTCCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
```

```
RESULT 5
AAH84970
ID AAH84970 standard; cDNA; 647 BP.
XX
XX AAH84970;
AC
XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P712P.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
FN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US030904.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.
XX
```

Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer.

Claim 5; Page 224; 325pp; English.

The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present invention

Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;

Query Match 100.0%; Score 646; DB 4; Length 647;  
Best Local Similarity 100.0%; Pred. No. 6.6e-200;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 60
DB 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 60
QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
```

```
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCGCCAAAGGTTCTATACAGGATATAA 120
QY 121 GGGGCTCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GGGGCTCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAATCTCTGACCTTTTGAACAGGCTTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAATCTCTGACCTTTTGAACAGGCTTACCTAATATCTG 240
QY 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTCTTACCATGAGGTTCTAGCTAAT 300
Db 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTCTTACCATGAGGTTCTAGCTAAT 300
QY 301 CTTGGCTTAAGATCTGGTTCCACATTAAGTTCTTGAATATGGGGGAAGGTTCAATTTGCT 360
Db 301 CTTGGCTTAAGATCTGGTTCCACATTAAGTTCTTGAATATGGGGGAAGGTTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAAGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAAGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GCGAACAATGGCTGAGCATATACCATAGGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
Db 421 GCGAACAATGGCTGAGCATATACCATAGGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
QY 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
Db 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
QY 541 GGCACCATTTGAGTGGCAACAATGCAGCAGCAGAGATCAATGGAACAACAAGATGATTC 600
Db 541 GGCACCATTTGAGTGGCAACAATGCAGCAGCAGAGATCAATGGAACAACAAGATGATTC 600
QY 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
```

```
RESULT 6
AAF86940
ID AAF86940 standard; cDNA; 647 BP.
XX
AC AAF86940;
XX
DT 06-JUL-2001 (first entry)
XX
DE Human P712P inventive antigen coding sequence SEQ ID NO: 335.
XX
KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
XX chromosome 11p13; zinc finger transcription factor; ss.
XX
OS Homo sapiens.
XX
PN WO200125273-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US027465.
XX
PR 04-OCT-1999; 99US-0157459P.
XX
PA (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
XX WPI; 2001-328324/34.
XX
PT Polypeptide comprising part of the Wilm's Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
XX and cancer associated with WT1.
XX
PS Disclosure; Page 214; 228pp; English.
```

```
XX The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WT1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WT1
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a coding sequence used in the exemplification of the invention
XX
SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
Query Match 100.0%; Score 646; DB 4; Length 647;
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCATTTTCATTATCATATGTAATCGGTCACCTCAAGGGGCCAACCCACAGCTGGAGCCAC 60
Db 1 AGCATTTTCATTATCATATGTAATCGGTCACCTCAAGGGGCCAACCCACAGCTGGAGCCAC 60
QY 61 TGTCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGATATAA 120
Db 61 TGTCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGATATAA 120
QY 121 GGGGCTCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GGGGCTCTCAGATATAGATCTGGTAGCAAGAAGAAACAAACACTGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTCTGACCCCTTTAGAAACAAGCTTAAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTCTGACCCCTTTAGAAACAAGCTTAAATATCTG 240
QY 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTCTTACCATGAGGTTCTAGCTAAT 300
Db 241 CTAGAGAAAGACCAACAGGCTCAAGGATCTCTTACCATGAGGTTCTAGCTAAT 300
QY 301 CTTGGCTTAAGATCTGGTTCCACATTAAGTTCTTGAATATGGGGGAAGGTTCAATTTGCT 360
Db 301 CTTGGCTTAAGATCTGGTTCCACATTAAGTTCTTGAATATGGGGGAAGGTTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAAGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAAGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420
QY 421 GCGAACAATGGCTGAGCATATACCATAGGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
Db 421 GCGAACAATGGCTGAGCATATACCATAGGATGCCCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 480
QY 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
Db 481 TGATCAATTTGCCATGAAGACTTGAGGACCTGAATCTACCGATTCATCTTAAGGCGAGCA 540
QY 541 GGCACCATTTGAGTGGCAACAATGCAGCAGCAGAGATCAATGGAACAACAAGATGATTC 600
Db 541 GGCACCATTTGAGTGGCAACAATGCAGCAGCAGAGATCAATGGAACAACAAGATGATTC 600
QY 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATGATAAAGGGGACCGT 647
RESULT 7
ACA59557
ID ACA59557 standard; cDNA; 647 BP.
XX
AC ACA59557;
XX
DT 10-JUN-2003 (first entry)
XX
XX Prostate cancer therapy associated cDNA #300.
DE Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
XX
```



KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;  
 KW PSMA; gene; ss.  
 XX Homo sapiens.  
 PN US2002192763-A1.  
 XX PD 19-DEC-2002.  
 XX 29-JUN-2001; 2001US-00895793.  
 XX PF 04-OCT-1999; 99US-0157455P.  
 XX PR 04-OCT-2000; 2000US-00679272.  
 XX PR 28-MAR-2001; 2001US-00822827.  
 XX (XUJ/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 PA (HURA/) HURAL J.  
 PA (MCNE/) MCNEILL P D.  
 PA (HOUG/) HOUGHTON R L.  
 PA (DBAS/) Y DE BASSOLS C V.  
 PA (FOYT/) FOY T W.  
 XX  
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;  
 PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;  
 XX WPI; 2001-245062/25.  
 DR  
 XX Prostate specific protein and its encoding polynucleotide, useful for the  
 PT treatment and diagnosis of prostate cancer.  
 PT  
 XX Example 3; SEQ ID NO 308; 85pp; English.  
 PS  
 CC The invention describes a fusion protein comprising at least one amino  
 CC acid sequence of immunogenic portions of any of the 3 sequences not  
 CC defined in the specification, or sequences having at least 70 or 90 %  
 CC sequence identity to any one of the 35 sequences defined in the USPTO web  
 CC site, which is encoded by any of the 4 nucleotide sequences not defined  
 CC in the specification. The fusion protein, composition and methods are  
 CC useful for diagnosing, preventing and/or treating cancer, particularly  
 CC prostate cancer. The proteins are useful as markers to indicate the  
 CC presence or absence of cancer. This sequence represents a prostate cancer  
 CC therapy associated cDNA. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from the US patent office at  
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763  
 XX  
 XX Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;  
 SQ  
 Query Match 100.0%; Score 646; DB 5; Length 647;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-200;  
 Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ACGATTTTCATTCATGTAATTCGGGTCACTCAAGGGGCCCAACACACAGCTGGAGCCAC 60  
 1 ACGATTTTCATTCATGTAATTCGGGTCACTCAAGGGGCCCAACACACAGCTGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120  
 Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120  
 Qy 121 GGNCCCTCACAGTATAGATCTGGTAGCAAGAAGAGAAACAAACACTGATCTCTTTCTG 180  
 Db 121 GGNCCCTCACAGTATAGATCTGGTAGCAAGAAGAGAGAAACAAACACTGATCTCTTTCTG 180  
 Qy 181 CCACCCCTTGACCCCTTTGGAACCTCTCTGACCCCTTTAGAACCAAGCCCTACCTAATCTG 240  
 Db 181 CCACCCCTTGACCCCTTTGGAACCTCTCTGACCCCTTTAGAACCAAGCCCTACCTAATCTG 240  
 Qy 241 CTAGAGAAAAGACCAACACGCGCTCAAGGATCTCTTACCAATCAAGGCTCTCAGCTAATT 300  
 Db 241 CTAGAGAAAAGACCAACACGCGCTCAAGGATCTCTTACCAATCAAGGCTCTCAGCTAATT 300  
 Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAAGGTTCTGAATATGGGGGCAAGGGTCAATTTGCT 360  
 Db 301 CTTGGCTAAGATGTGGGTTCCACATTAAGGTTCTGAATATGGGGGCAAGGGTCAATTTGCT 360  
 Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGACGAGGGGGCTGCTTGTCTTT 420  
 Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGACGAGGGGGCTGCTTGTCTTT 420  
 Qy 421 GGGNACAATGGCTGAGCATATTAACCATAGGTTTATGGGGAAACAAACACATCAAGTCAC 480  
 Db 421 GGGNACAATGGCTGAGCATATTAACCATAGGTTTATGGGGAAACAAACACATCAAGTCAC 480  
 Qy 481 TGTATCAATTGCCATGAAGACTTTGAGGGAACCTGAATCTACCGATTCTTTAAGGCAGCA 540  
 Db 481 TGTATCAATTGCCATGAAGACTTTGAGGGAACCTGAATCTACCGATTCTTTAAGGCAGCA 540  
 Qy 541 GGACCAAGTTTGAAGTGGCAACAATGTCAGCAGCAGCAATCAATGCGAAAACACAGATGATGC 600  
 Db 541 GGACCAAGTTTGAAGTGGCAACAATGTCAGCAGCAGCAATCAATGCGAAAACACAGATGATGC 600  
 Qy 601 AATGTCCTTTTTTTTCTCTCTGCTTCTGACCTTGATTAAGGGGACCGT 647  
 Db 601 AATGTCCTTTTTTTTCTCTCTGCTTCTGACCTTGATTAAGGGGACCGT 647  
 .  
 RESULT 8  
 ABL95120  
 ID ABL95120 standard; cDNA; 647 BP.  
 XX  
 XX ABL95120;  
 XX  
 XX 19-JUL-2002 (first entry)  
 DT  
 XX Human P712P cDNA sequence SEQ ID NO 308.  
 DE  
 XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;  
 KW gene therapy; gene; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US2002022248-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 PF 12-JAN-2001; 2001US-00759143.  
 XX  
 XX 25-FEB-1997; 97US-00806099.  
 PR 01-AUG-1997; 97US-00904804.  
 PR 10-FEB-1998; 98US-00020956.  
 PR 25-FEB-1998; 98US-00030607.  
 PR 14-JUL-1998; 98US-00115453.  
 PR 23-SEP-1998; 98US-00159812.  
 PR 15-JAN-1999; 99US-00232149.  
 PR 09-APR-1999; 99US-00288946.  
 PR 13-JUL-1999; 99US-00352616.  
 PR 12-NOV-1999; 99US-00439313.



CC	illustrate the invention	
XX		
SQ	Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;	
	Query Match	
	Best Local Similarity 100.0%; Score 646; DB 8; Length 647;	
	Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ACGATTTTCATATCATGTAATCGGTGCTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60	
Db		
QY	1 ACGATTTTCATATCATGTAATCGGTGCTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60	
Db		
QY	61 TGCTCAGGGGAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120	
Db		
QY	61 TGCTCAGGGGAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120	
Db		
QY	121 GNGGCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACCTGATCTCTTCTG 180	
Db		
QY	121 GNGGCTCACAGTATAGATCTGGTAGCAAGAAAGAAACAAACACCTGATCTCTTCTG 180	
Db		
QY	181 CCACCCCTCGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240	
Db		
QY	181 CCACCCCTCGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240	
Db		
QY	241 CTAGAGAAAGACCAACACCGCCTCAAGGATCTTTACCATGAAGTCTCAGCTAATT 300	
Db		
QY	241 CTAGAGAAAGACCAACACCGCCTCAAGGATCTTTACCATGAAGTCTCAGCTAATT 300	
Db		
QY	301 CTTGCTTAAGATGTGGTTCACATTTAGTTCCTGAATATGGGGGAAGGTCATTTGCT 360	
Db		
QY	301 CTTGCTTAAGATGTGGTTCACATTTAGTTCCTGAATATGGGGGAAGGTCATTTGCT 360	
Db		
QY	361 CATTTTGTGTGTAAGTCCAGATGCCAGGGGCCAGAGCGGGCTGCTTGCTTT 420	
Db		
QY	361 CATTTTGTGTGTAAGTCCAGATGCCAGGGGCCAGAGCGGGCTGCTTGCTTT 420	
Db		
QY	421 GGGAAACAATGGCTGAGCATATTAACATAGTTATGGGGAACAAACATCAAGTCTAC 480	
Db		
QY	421 GGGAAACAATGGCTGAGCATATTAACATAGTTATGGGGAACAAACATCAAGTCTAC 480	
Db		
QY	481 TGTATCAATTGGCATGAAGACTTTGAGGACCTGAATCTACCATTTAAGGCAGCA 540	
Db		
QY	481 TGTATCAATTGGCATGAAGACTTTGAGGACCTGAATCTACCATTTAAGGCAGCA 540	
Db		
QY	541 GGACAGTTTGATGGCAACAATGCAGCAGCAGAGATCAATGAAACAAACAGAAATGTC 600	
Db		
QY	541 GGACAGTTTGATGGCAACAATGCAGCAGCAGAGATCAATGAAACAAACAGAAATGTC 600	
Db		
QY	601 ATGTCCCTTTTCTCTGCTTCTGACTTGATTAAGGGGACCGT 647	
Db		
QY	601 ATGTCCCTTTTCTCTGCTTCTGACTTGATTAAGGGGACCGT 647	
Db		
XX	RESULT 10	
XX	ADBI3758	
ID	ADBI3758 standard; cDNA; 647 BP.	
XX		
AC	ADBI3758;	
XX		
DT	18-DEC-2003 (first entry)	
XX		
DE	Human prostate specific cDNA P7112P.	
XX		
KW	Human; ss; prostate specific cDNA; cytostatic; immunostimulant;	
KW	Gene therapy; cell therapy; vaccine; T-cell epitope;	
KW	Class I major histocompatibility complex allele; MHC; prostate cancer;	
KW	tumour; antigen presenting cell.	
XX		
OS	Homo sapiens.	
XX		
PN	US2003185830-A1.	
XX		
PD	02-OCT-2003.	

XX	12-NOV-2002; 2002US-00294025.	
PF		
XX	25-FEB-1997; 97US-00806099.	
XX	01-AUG-1997; 97US-00904804.	
PR	09-FEB-1998; 98US-00020956.	
PR	25-FEB-1998; 98US-00030607.	
PR	14-JUL-1998; 98US-00115453.	
PR	23-SEP-1998; 98US-00159812.	
PR	15-JAN-1999; 99US-00232149.	
PR	09-APR-1999; 99US-00288946.	
PR	13-JUL-1999; 99US-00352616.	
PR	12-NOV-1999; 99US-00439313.	
PR	18-NOV-1999; 99US-00443686.	
PR	14-JAN-2000; 2000US-00483672.	
PR	27-MAR-2000; 2000US-00536857.	
PR	09-MAY-2000; 2000US-00568100.	
PR	12-MAY-2000; 2000US-00570737.	
PR	13-JUN-2000; 2000US-00593793.	
PR	27-JUN-2000; 2000US-00605783.	
PR	09-AUG-2000; 2000US-00636215.	
PR	29-AUG-2000; 2000US-00651236.	
PR	06-SEP-2000; 2000US-00657279.	
PR	02-OCT-2000; 2000US-00679426.	
PR	10-OCT-2000; 2000US-00685166.	
PR	09-NOV-2000; 2000US-00709729.	
PR	12-JAN-2001; 2001US-00759143.	
PR	09-FEB-2001; 2001US-00780669.	
PR	09-MAY-2001; 2001US-00852911.	
PR	29-JUN-2001; 2001US-00895814.	
PR	10-DEC-2001; 2001US-00012896.	
PR	09-MAY-2002; 2002US-00144678.	
XX	(CORI-) CORIXA CORP.	
PA		
XX	Xu J, Stolck JA, Kalos MD;	
PI	WPI; 2003-756193/71.	
XX		
DR		
XX		
PT	New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer.	
PT		
PT		
XX		
PS	Example 3; Page; 101pp; English.	
XX		
CC	The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The	
CC	peptides comprise a fragment ADBI3563 of that contain naturally processed	
CC	T-cell epitopes for 3 class I major histocompatibility complex (MHC)	
CC	alleles. ADBI3563 is a polypeptide encoded by a human prostate specific	
CC	cDNA, one of 648 disclosed as new. Also included are nucleic acids	
CC	encoding the proteins and peptides, expression vectors, a host cell	
CC	transformed with the vector, an isolated antibody (or antigen binding	
CC	fragment) that specifically binds to the protein or peptide, detecting	
CC	the presence of a cancer in a patient (comprising contacting a patient	
CC	sample with a binding agent that binds to the peptides or a polypeptide	
CC	appearing as ADBI3558, detecting the amount of polypeptide that binds to	
CC	the agent and comparing the amount of polypeptide to a predetermined cut-	
CC	off value to determine the presence of cancer), a fusion protein	
CC	comprising the peptides or proteins, stimulating or expanding T cells	
CC	specific for a tumour protein comprising contacting T cells with the	
CC	peptides or the isolated T cell population, treating prostate cancer in a	
CC	patient comprising administering a composition comprising the peptides,	
CC	nucleic acids, antibodies or compounds, determining the presence of a	
CC	cancer in a patient and treating prostate cancer in a patient comprising	
CC	incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated	
CC	from a patient with the peptides or antigen presenting cells that express	
CC	(the peptides so that the T cells proliferate, and administering the	
CC	proliferated T cells to the patient. The peptides (or an oligonucleotide	
CC	that hybridises to nucleic acid encoding them), is used to detect the	
CC	presence of cancer in a patient. The peptides, nucleic acids encoding, or	
CC	antigen-presenting cells expressing the nucleic acid, are used to	
CC	stimulate or expand T cells specific for a tumour protein. The peptides,	

nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is one of the disclosed human prostate specific cDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.

```
Query Match      100.0%; Score 646; DB 10; Length 647;
Best Local Similarity 100.0%; Pred. NO. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACCAACGCTGGAGCCAC	60
Db	1	ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGGCCAACCAAGCTGGAGCCAC	60
Qy	61	TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA	120
Db	61	TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA	120
Qy	121	GGNGCCTCACAGTATAGATCTGTGTAGCAAAAGAGAGAAACAAACACTGATCTCTTTCTGTG	180
Db	121	GGNGCCTCACAGTATAGATCTGTGTAGCAAAAGAGAGAAACAAACACTGATCTCTCTTTCTGTG	180
Qy	181	CCACCCCTCTGACCCCTTTTGGAACTCCTCTGACCCCTTTAGAACAAAGCCCTACTTAATATCTG	240
Db	181	CCACCCCTCTGACCCCTTTTGGAACTCCTCTGACCCCTTTAGAACAAAGCCCTACTTAATATCTG	240
Qy	241	CTAGAGAAAGAACCAACAGCCCTCAAGGATCTCTTACATCAAGGTCCTCAGCTAAATT	300
Db	241	CTAGAGAAAGAACCAACAGCCCTCAAGGATCTCTTACATCAAGGTCCTCAGCTAAATT	300
Qy	301	CTTGGCTAAGATGTGGGTTTCCACATTAGTGTCTGAATATATGGGGGAAGGGTCAATTTGCT	360
Db	301	CTTGGCTAAGATGTGGGTTTCCACATTAGTGTCTGAATATATGGGGGAAGGGTCAATTTGCT	360
Qy	361	CATTTTGTGTGGATAAAGTCAGAGTCCCCAGGGGCCAGAGCAGGGGGCTGCTTCGCTTTT	420
Db	361	CATTTTGTGTGGATAAAGTCAGAGTCCCCAGGGGCCAGAGCAGGGGGCTGCTTCGCTTTT	420
Qy	421	GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGGAACAAAACAACATCAAGCTCAC	480
Db	421	GGGAACAATGGCTGAGCATATAAACCATAGGTTATGGGGGAACAAAACAACATCAAGCTCAC	480
Qy	481	TGTATCAATTGCCATGAAGACTTGAGGGAACCTGAATCTACCGATTCAATCTTAAGGGCAGCA	540
Db	481	TGTATCAATTGCCATGAAGACTTGAGGGAACCTGAATCTACCGATTCAATCTTAAGGGCAGCA	540
Qy	541	GGACCAAGTTTGAGTGGCAACAATGCAGCAGCAGAAATCAATGGGAAAACAACAGATGATTCG	600
Db	541	GGACCAAGTTTGAGTGGCAACAATGCAGCAGCAGAAATCAATGGGAAAACAACAGATGATTCG	600
Qy	601	AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGTATATAAAGGGGACCGT	647
Db	601	AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGTATATAAAGGGGACCGT	647

## RESULT 11

RESUL I.  
ADG26174

ADG26174  
ID ADG26174 standard; cDNA; 647 BP.

XX

AC ADG26174;

XX

DT 26-FEB-2004 (first entry)

DE Human prostate-specific cD

XXI

KW Human; prostate-specific p

[illegible]

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
XX Carlos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;  
PI Pi Kates D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
PI McNeill PD, Houghton RL, Vinals Y De Bassolec, Foy TW, Watanabe Y;  
PI Meagher MJ, Deng T;  
XX  
XX WPI: 2003-777973/73.  
DR

PT New polynucleotides encoding prostate specific polypeptides isolated from  
PT a human prostate tumor cDNA library are useful to diagnose and treat  
PT cancer particularly prostate cancer.

Example 3: SEO ID NO 308: 99pp: English:

The invention relates to human prostate-specific polypeptides and the polynucleotides encoding them. The invention also relates to an isolated antibody or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide compared to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents cDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at [sedata.uspto.gov/sequence.html](http://sedata.uspto.gov/sequence.html).

Sequence 647 BP: 190 A: 141 C: 154 G: 161 T: 0 U: 1 Other;

Query Match 100.0%: Score 646: DB 10: Length 647;

Query Match	100.0%;	Score 0.10;	25.10;
Best Local Similarity	100.0%;	Pred. No. 6.6e-200;	

Local similarity: 100.00; Local identity: 100.00  
 Matches: 647; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACAGCTGGGAGCCAC 60

Db 1 ACGATTTTCATATCATGTAAATCGGTCACCTCAAGGGGCCACCAACAGCTGGGAGCCAC 60  
Qy 61 TGCTCAGGGGAAGTTTCATATATGGGACTTTCTACTGCCCAAGTTCTTATACAGGATATAAA 120  
Db 61 TGCTCAGGGGAAGTTTCATATATGGGACTTTCTACTGCCCAAGTTCTTATACAGGATATAAA 120  
Qy 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAAACAAACACATGATCTCTTTCTG 180  
Db 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAAACAAACACATGATCTCTTTCTG 180  
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240  
Db 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240  
Qy 241 CTAGAGAAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300  
Db 241 CTAGAGAAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300  
Qy 301 CTTGGCTAAGATGTGGTTTCCATAGTTCTGAATATGGGGGAAGGTCATTTGCT 360  
Db 301 CTTGGCTAAGATGTGGTTTCCATAGTTCTGAATATGGGGGAAGGTCATTTGCT 360  
Qy 361 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420  
Db 361 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420  
Qy 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACAAACATCAAGTCTAC 480  
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACAAACATCAAGTCTAC 480  
Qy 481 TGTATCAATTCGCATGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 540  
Db 481 TGTATCAATTCGCATGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 540  
Qy 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAACAACAAGATGATTGC 600  
Db 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAACAACAAGATGATTGC 600  
601 AATGTCCTTTTCTCTGCTCTGCTTCTGATTAAGGGGACCGT 647  
601 AATGTCCTTTTCTCTGCTCTGCTTCTGATTAAGGGGACCGT 647  
RESULT 12  
ID AEF66455  
XX AEF66455 standard; cDNA; 647 BP.  
AC AEF66455;  
XX  
XX  
DT 06-APR-2006 (first entry)  
XX  
DE Human prostate tumor cDNA clone P712P, SEQ ID 308.  
XX  
XX Cytostatic; Gene Therapy; prostate tumor; ss.  
OS Homo sapiens.  
XX  
XX US2006024301-A1.  
XX  
XX 02-FEB-2006.  
XX  
XX 23-SEP-2005; 2005US-00234786.  
XX  
XX 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 09-FEB-1996; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
PR 14-JUL-1998; 98US-00115453.  
PR 23-SEP-1998; 98US-00159812.  
PR 15-JAN-1999; 99US-00232149.  
PR 09-APR-1999; 99US-00288946.  
PR 13-JUL-1999; 99US-00352616.

PR 12-NOV-1999; 99US-00439313.  
PR 18-NOV-1999; 99US-00443686.  
PR 14-JAN-2000; 2000US-00483672.  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PA (CORI-) CORIXA CORP.  
XX  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick IS;  
PI Carter D, Li SX, Wang A, Skeiky YAW;  
XX  
XX WPI; 2006-117603/12.  
XX  
XX New fusion protein comprising a p50S polypeptide and an unrelated fusion  
PT partner, useful for diagnosing, preventing, or treating cancer, such as  
PT prostate cancer.  
XX  
XX Example 3; SEQ ID NO 308; 78pp; English.  
XX  
XX The present invention relates to prostate-specific fusion proteins and  
CC DNA encoding sequences. The fusion proteins can be used for diagnosing,  
CC preventing, or treating cancer, such as prostate cancer. The prostate-  
CC specific proteins were isolated from a human prostate tumor cDNA library.  
CC The present sequence is one such cDNA clone which was isolated in the  
CC prostate-specific cDNA library. Note: The sequence data for this patent  
CC did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;  
Query Match 100.0%; Score 646; DB 15; Length 647;  
Best Local Similarity 100.0%; Pred. No. 6.6e-200; Indels 0; Gaps 0;  
Matches 647; Conservative 0; Mismatches 0;  
Qy 1 ACGATTTTCATATCATGTAAATCGGTCACCTCAAGGGGCCCAACACAGCTGGGAGCCAC 60  
Db 1 ACGATTTTCATATCATGTAAATCGGTCACCTCAAGGGGCCCAACACAGCTGGGAGCCAC 60  
Qy 61 TGCTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGTTCTTATACAGGATATAAA 120  
Db 61 TGCTCAGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGTTCTTATACAGGATATAAA 120  
Qy 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAAACAAACACATGATCTCTTTCTG 180  
Db 121 GGNGCCTCACAGTATAGATCTGGTATAGCAAGAGAGAGAAACAAACACATGATCTCTTTCTG 180  
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240  
Db 181 CCACCCCTCTGACCCCTTTGGAACTCCTCTGACCCCTTTAGAACCAAGCTACCTAATATCTG 240  
Qy 241 CTAGAGAAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300  
Db 241 CTAGAGAAAAGACCAACAGCCCTCAAGGATCTCTTACCATGAAGTCTCAGCTAATT 300  
Qy 301 CTTGGCTAAGATGTGGTTTCCATAGTTCTGAATATGGGGGAAGGTCATTTGCT 360  
Db 301 CTTGGCTAAGATGTGGTTTCCATAGTTCTGAATATGGGGGAAGGTCATTTGCT 360  
Qy 361 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420  
Db 361 CATTTTGTGTGGATAAGTCAGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGTCTT 420  
Qy 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACAAACATCAAGTCTAC 480  
Db 421 GGGAAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAACAAACATCAAGTCTAC 480  
Qy 481 TGTATCAATTCGCATGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 540  
Db 481 TGTATCAATTCGCATGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 540  
Qy 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAACAACAAGATGATTGC 600  
Db 541 GGACAGTTTGTAGTGGCAACAATGAGCAGCAGAGATCAATGGAACAACAAGATGATTGC 600

Db 541 GGACCACTTTGAGTGGCAACAATGACAGCAGCAATCAATGGAACACAGAGATGATTC 600  
 QY 601 AATGTCCTTTTCTCTGCTTCTGACTTGATATAAGGGGACCGT 647  
 Db 601 AATGTCCTTTTCTCTGCTTCTGACTTGATATAAGGGGACCGT 647

RESULT 13  
 ID ADB14484  
 XX ADB14484 standard; cDNA; 2577 BP.  
 AC ADB14484;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX Human prostate antigen P712P additional DNA sequence.  
 XX Human, ss; prostate specific cDNA; cytostatic; immunostimulant;  
 KW gene therapy; cell therapy; vaccine; T-cell epitope;  
 KW class I major histocompatibility complex allele; MHC; prostate cancer;  
 KW tumour; antigen presenting cell.  
 XX Homo sapiens.  
 OS  
 XX  
 PN US2003185830-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 XX 12-NOV-2002; 2002US-00294025.  
 XX 25-FEB-1997; 97US-00806099.  
 PR 01-AUG-1997; 97US-00904804.  
 PR 09-FEB-1998; 98US-00020956.  
 PR 25-FEB-1998; 98US-00030607.  
 PR 14-JUL-1998; 98US-00115453.  
 PR 23-SEP-1998; 98US-00159812.  
 PR 15-JAN-1999; 99US-00232149.  
 PR 09-APR-1999; 99US-00288946.  
 PR 13-JUL-1999; 99US-00352616.  
 PR 12-NOV-1999; 99US-00439313.  
 PR 18-NOV-1999; 99US-00443686.  
 PR 14-JAN-2000; 2000US-00483672.  
 PR 27-MAR-2000; 2000US-00536857.  
 PR 09-MAY-2000; 2000US-00568100.  
 PR 12-MAY-2000; 2000US-00570737.  
 PR 13-JUN-2000; 2000US-00593793.  
 PR 27-JUN-2000; 2000US-00605783.  
 PR 09-AUG-2000; 2000US-00636215.  
 PR 29-AUG-2000; 2000US-00651236.  
 PR 06-SEP-2000; 2000US-00657279.  
 PR 02-OCT-2000; 2000US-00679426.  
 PR 10-OCT-2000; 2000US-00685166.  
 PR 09-NOV-2000; 2000US-00709729.  
 PR 12-JAN-2001; 2001US-00759143.  
 PR 09-FEB-2001; 2001US-00780669.  
 PR 09-MAY-2001; 2001US-00852911.  
 PR 29-JUN-2001; 2001US-00895814.  
 PR 10-DEC-2001; 2001US-00012896.  
 PR 09-MAY-2002; 2002US-00144678.  
 XX (CORI-) CORIXA CORP.  
 XX  
 XX Xu J, Stolk JA, Kalos MD;  
 XX WPI; 2003-756193/71.  
 XX  
 PT New isolated polypeptide for use in a vaccine for stimulating an immune  
 PT response, or for treating or diagnosis cancer, preferably prostate  
 PT cancer.  
 XX  
 PS Claim 6; Page; 101pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide comprising no more than

CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The  
 CC peptide comprise a fragment ADB13563 of that contain naturally processed  
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)  
 CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific  
 CC cDNA, one of 648 disclosed as new. Also included are nucleic acids  
 CC encoding the proteins and peptides, expression vectors, a host cell  
 CC transformed with the vector, an isolated antibody (or antigen binding  
 CC fragment) that specifically binds to the protein or peptide, detecting  
 CC the presence of a cancer in a patient (comprising contacting a patient  
 CC sample with a binding agent that binds to the peptides or a polypeptide  
 CC appearing as ADB13563, detecting the amount of polypeptide that binds to  
 CC the agent and comparing the amount of polypeptide to a predetermined cut-  
 CC off value to determine the presence of cancer), a fusion protein  
 CC comprising the peptides or proteins, stimulating or expanding T cells  
 CC specific for a tumour protein comprising contacting T cells with the  
 CC peptide or the isolated T cell population, treating prostate cancer in a  
 CC patient comprising administering a composition comprising the peptides,  
 CC nucleic acids, antibodies or compounds, determining the presence of a  
 CC cancer in a patient and treating prostate cancer in a patient comprising  
 CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated  
 CC from a patient with the peptides or antigen presenting cells that express  
 CC (the peptides so that the T cells proliferate, and administering the  
 CC proliferated T cells to the patient. The peptides (or an oligonucleotide  
 CC that hybridises to nucleic acid encoding them), is used to detect the  
 CC presence of cancer in a patient. The peptides, nucleic acids encoding, or  
 CC antigen-presenting cells expressing the nucleic acid, are used to  
 CC stimulate or expand T cells specific for a tumour protein. The peptides,  
 CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen  
 CC presenting cells are used to stimulate an immune response or treat  
 CC prostate cancer in a patient. The present sequence is a known cDNA  
 CC showing sequence similarity to one of the disclosed human prostate  
 CC specific cDNAs. Note: Except where otherwise indicated, the sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030185830.  
 XX

SQ Sequence 2577 BP; 826 A; 537 C; 506 G; 708 T; 0 U; 0 Other;

Query Match 93.0%; Score 600.8; DB 10; Length 2577;  
 Best Local Similarity 98.1%; Pred. No. 8e-185;  
 Matches 629; Conservative 0; Mismatches 8; Indels 4; Gaps 2;

QY 1 ACGATTTTCATTATCATGTCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 60  
 Db 636 ACGATTTTCATTATCATGTCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 695

QY 61 TGTCTAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTCTTACAGGATATAAA 120  
 Db 696 TGTCTAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGTTCTTACAGGATATAAA 755

QY 121 GGNGCCTCACAGTATAGATCTGGTACAAAGAGAGAAACAAACACTGATCTCTTCTG 180  
 Db 756 GGTGCTTCACAGTATAGATCTGGTACAAAGAGAGAAACAAACACTGATCTCTTCTG 815

QY 181 CCACCCCTCTGACCCCTTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTATATCTG 240  
 Db 816 CCACCCCTCTGACCCCTTTTGGAACTCCTCTGACCCCTTTAGAACAGCCCTACCTATATCTG 875

QY 241 CTAGAGAAAAGACCAACAAACCGCTTCAAGAGATCTTTTACCATGAAGGTTCTCAGCTAATT 300  
 Db 876 CTAGAGAAAAGACCAACAAACCGCTTCAAGAGATCTTTTACCATGAAGGTTCTCAGCTAATT 935

QY 301 CTTGCTAAGATGTGGTTTCCACATTAGTTCGTGAATATGGGGGAGAGGTCATTTGCT 360  
 Db 936 CTTGCTAAGATGTGGTTTCCACATTAGTTCGTGAATATGGGGGAGAGGTCATTTGCT 995

QY 361 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGAGGGGGCTCTCTGCTTT 420  
 Db 996 CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGAGGGGGCTCTCTGCTTT 1054

QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAAACAACATCAAGTCAC 480  
 Db 1055 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAAACAACATCAAGTCAC 1111





PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1; Page 3587; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX

SQ Sequence 1481 BP; 364 A; 346 C; 314 G; 453 T; 0 U; 4 Other;

Query Match 92.8%; Score 599.2; DB 5; Length 1481;

Best Local Similarity 98.0%; Pred. No. 2e-184;

Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

QY 1 ACGATTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60

DB 1097 ACGATTTTCATTATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 1038

QY 61 TGTCTAGGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

DB 1037 TGTCTAGGGGGAAGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 978

QY 121 GNGCCTCAGTATAGATCTGTAGCAAGAAGAAGAAACAAACACTGATCTCTTTCTG 180

DB 977 GGTGCTCAGTATAGATCTGTAGCAAGAAGAAGAAACAAACACTGATCTCTTTCTG 918

QY 181 CCACCCCTCTGACCTTTGGAACTCTCTGACCTTTAGAAACAAAGCTACCTAAATCTG 240

DB 917 CCACCCCTCTGACCTTTGGAACTCTCTGACCTTTAGAAACAAAGCTACCTAAATCTG 858

QY 241 CTAGAGAAAGACCAACAAAGGCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAAT 300

DB 857 CTAGAGAAAGACCAACAAAGGCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAAT 798

QY 301 CTTGGCTAAGATGTGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 360

DB 797 CTTGGCTAAGATGTGGTTCCACATTAGGTTCTGAATATGGGGGAAGGTCATTTGCT 738

QY 361 CATTGTGTGTGTAATAGTCCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTGCTTT 420

DB 737 CATTGTGTGTGTAATAGTCCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTGCTTT 679

QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAAACAAACATCAAGTCTAC 480

DB 678 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGGAAACAAACATCAAGTCTAC 622

QY 481 TGTATCAATTTGCAATGAAGCTTGGGACCTGAATCTACCGATTCATTTAAGGCAGCA 540

DB 621 TGTATCAATTTGCAATGAAGCTTGGGACCTGAATCTACCGATTCATTTAAGGCAGCA 562

QY 541 GGACCAATTTGAGTGGCAACATGACAGCAGAGATCAATGGAAACAACAGATGATTC 600

DB 561 GGACCAATTTGAGTGGCAACATGACAGCAGAGATCAATGGAAACAACAGATGATTC 502

QY 601 AATGTCCTTTTCTCTCTGCTTCTGACTTGATAAAGGG 641

DB 501 AATGTCCTTTTCTCTCTGCTTCTGACTTGATAAAGGG 461

Search completed: December 31, 2006, 12:54:16

Job time : 504.906 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
9932.518 Million cell updates/sec

Title: US-09-232-880-308

Perfect score: 646

Sequence: 1 acgatttcattcatcatgta.....acttgataaaaggagccgt 647

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
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5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	100.0	647	2	BD242213
2	646	100.0	647	2	AR237396
3	646	100.0	647	2	AR278420
4	646	100.0	647	2	AR367116
5	646	100.0	647	2	AR371012
6	646	100.0	647	2	AR400152
7	646	100.0	647	2	AR405419
8	646	100.0	647	2	AR439623
9	646	100.0	647	2	AR563799
10	646	100.0	647	2	AR588785
11	646	100.0	647	2	AR605605
12	646	100.0	647	2	AR656944
13	646	100.0	647	2	AR716851
14	646	100.0	647	2	AX106197
15	646	100.0	647	2	AX106527
16	646	100.0	647	2	AX140818
17	646	100.0	647	2	AX200678
18	646	100.0	647	2	AX267334

19	602.4	93.3	1270	5	AY458019	Homo sapi
20	600.8	93.0	2084	5	AK056884	Homo sapi
21	600.8	93.0	2577	5	AY338953	Homo sapi
22	600.8	93.0	154078	5	CN507BFD	Human chr
23	599.2	92.8	1481	2	CQ489609	Sequence
24	599.2	92.8	1481	2	CQ489669	Sequence
25	599.2	92.8	1481	2	CQ489695	Sequence
26	599.2	92.8	1481	2	CQ489711	Sequence
27	599.2	92.8	1481	2	CQ490222	Sequence
28	599.2	92.8	1481	2	CQ493912	Sequence
29	599.2	92.8	1481	2	CQ495511	Sequence
30	599.2	92.8	1481	2	CQ495537	Sequence
31	599.2	92.8	1481	2	CQ496084	Sequence
32	599.2	92.8	2577	2	AR278594	Sequence
33	599.2	92.8	2577	2	AR400326	Sequence
34	599.2	92.8	2577	2	AR405593	Sequence
35	599.2	92.8	2577	2	AR563973	Sequence
36	599.2	92.8	2577	2	AR588959	Sequence
37	599.2	92.8	2577	2	AR605779	Sequence
38	599.2	92.8	2577	2	AR657118	Sequence
39	599.2	92.8	2577	2	AR717025	Sequence
40	599.2	92.8	2577	2	AX200922	Sequence
41	599.2	92.8	2577	2	AX267578	Sequence
42	599.2	92.8	37981	5	AP000529	Homo sapi
43	599.2	92.8	42225	5	CR545463	Human DNA
44	599.2	92.8	176156	5	CNS080CG	Human chr
45	583.4	90.3	813	7	BV557845	pzr63f03.

## ALIGNMENTS

BD242213	647 bp	DNA	linear	PAT 17-JUL-2003
Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.				
BD242213				
BD242213.1	GI:33051983			
JP 2002520054-A/300.				
Homo sapiens				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
OS	Homo sapiens (human)			
PN	JP 2002520054-A/300			
PD	09-JUL-2002			
PF	14-JUL-1999	JP 2000560247		
PR	14-JUL-1998	US 09/115453,14-JUL-1998	US 09/116134	PR
23-SEP-1998	US 09/159822,23-SEP-1998	US 09/159812	PR	
15-JAN-1999	US 09/232880,15-JAN-1999	US 09/232149	PR	
09-APR-1999	US 09/288946			
PI	DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI			
JIANGCHUN XU,				
PI	JENNIFER LYNN MITCHAM			
PC	CI2N15/09,A61K39/00,A61K39/395,C07K14/47,C07K16/30,			
PC	CI2N5/10,			
PC	CI2P21/08,CI2Q1/68,G01N33/574,G01N33/68//A61P35/00,CI2N15/00,			
PC	A61K37/02,			
PC	CI2N5/00			
CC	n = A,T,C or G			
PH	Key	Location/Qualifiers		
FT	misc	Location (1) . (647).		
source				
1. .647				
/organism="Homo sapiens"				



ORIGIN		/mol_type="genomic DNA"	
Query Match		100.0%; Score 646; DB 2; Length 647;	
Best Local Similarity		100.0%; Pred. No. 7.6e-202;	
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC	60
DB	1	ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC	60
QY	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCAGGTTCTATACAGGATATAA	120
DB	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCAGGTTCTATACAGGATATAA	120
QY	121	GGNGCCTCAGATATAGATCTGGTAGCAAGAGAGAGAACAAACACTGATCTCTTCTG	180
DB	121	GGNGCCTCAGATATAGATCTGGTAGCAAGAGAGAGAACAAACACTGATCTCTTCTG	180
QY	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
DB	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
QY	241	CTAGAGAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
DB	241	CTAGAGAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
QY	301	CTTGCTTAAGATGTGGTTTCCACATTAAGTCTCTGATATGGGGGAGGTCATTTGCT	360
DB	301	CTTGCTTAAGATGTGGTTTCCACATTAAGTCTCTGATATGGGGGAGGTCATTTGCT	360
QY	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
DB	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
QY	421	GGGAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACAACATCAAGTCTAC	480
DB	421	GGGAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACAACATCAAGTCTAC	480
QY	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
DB	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
QY	541	GGACCAAGTTTGTAGTGGCAACATGCAGCAGCAAGATCAATGGAACAAACAGAGATGTC	600
DB	541	GGACCAAGTTTGTAGTGGCAACATGCAGCAGCAAGATCAATGGAACAAACAGAGATGTC	600
QY	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647
DB	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647
RESULT 5			
AR371012		647 bp DNA linear PAT 12-SEP-2003	
LOCUS		Sequence 308 from patent US 6395278.	
DEFINITION		AR371012	
ACCESSION		AR371012.1	
VERSION		GI:34607905	
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 647)	
AUTHORS		Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yuqiu, J.,	
TITLE		Prostate specific fusion protein compositions	
JOURNAL		Patent: US 6395278-A 308 28-MAY-2002;	
FEATURES		Corixa Corporation; Seattle, WA	
source		1..647	
ORIGIN		/mol_type="genomic DNA"	

ORIGIN		/mol_type="genomic DNA"	
Query Match		100.0%; Score 646; DB 2; Length 647;	
Best Local Similarity		100.0%; Pred. No. 7.6e-202;	
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC	60
DB	1	ACGATTTTCATTATCATGTAAATCGGTCACCTCAAGGGGCCAACACAGCTGGAGCCAC	60
QY	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCAGGTTCTATACAGGATATAA	120
DB	61	TGCTCAGGGGAAGGTTCAATATGGGACTTTCTACTGCCCAGGTTCTATACAGGATATAA	120
QY	121	GGNGCCTCAGATATAGATCTGGTAGCAAGAGAGAGAACAAACACTGATCTCTTCTG	180
DB	121	GGNGCCTCAGATATAGATCTGGTAGCAAGAGAGAGAACAAACACTGATCTCTTCTG	180
QY	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
DB	181	CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACCTAATATCTG	240
QY	241	CTAGAGAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
DB	241	CTAGAGAAAGACCAACACCGGCTCAAAGGATCTCTTACCATGAAGGTTCTCAGCTAAT	300
QY	301	CTTGCTTAAGATGTGGTTTCCACATTAAGTCTCTGATATGGGGGAGGTCATTTGCT	360
DB	301	CTTGCTTAAGATGTGGTTTCCACATTAAGTCTCTGATATGGGGGAGGTCATTTGCT	360
QY	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
DB	361	CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTCTTT	420
QY	421	GGGAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACAACATCAAGTCTAC	480
DB	421	GGGAACAATGGCTGAGCATATAACCATAGTTTATGGGGAACAAAACAACATCAAGTCTAC	480
QY	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
DB	481	TGTATCAATGGCCATGAAGACTTGAAGGACCTGAATCTACCGATTCATCTTAAGGAGCA	540
QY	541	GGACCAAGTTTGTAGTGGCAACATGCAGCAGCAAGATCAATGGAACAAACAGAGATGTC	600
DB	541	GGACCAAGTTTGTAGTGGCAACATGCAGCAGCAAGATCAATGGAACAAACAGAGATGTC	600
QY	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647
DB	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647
RESULT 4			
AR367116		647 bp DNA linear PAT 12-SEP-2003	
LOCUS		Sequence 308 from patent US 6329505.	
DEFINITION		AR367116	
ACCESSION		AR367116.1	
VERSION		GI:34600091	
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 647)	
AUTHORS		Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yuqiu, J.,	
TITLE		Compositions and methods for therapy and diagnosis of prostate	
JOURNAL		Patent: US 6329505-A 308 11-DEC-2001;	
FEATURES		Corixa Corporation; Seattle, WA	
source		1..647	
ORIGIN		/organism="unknown"	

Query Match 100.0%; Score 646; DB 2; Length 647;  
Best Local Similarity 100.0%; Pred. No. 7.6e-202; Indels 0; Gaps 0;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60  
DB 1 ACGATTTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120  
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120

QY 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTCTG 180  
DB 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTCTG 180

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240  
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

QY 241 CTAGAGAAAAGACCAACACCGGCTCAAGGATCTTTACCATGAAGGTTCTCAGCTAATT 300  
DB 241 CTAGAGAAAAGACCAACACCGGCTCAAGGATCTTTACCATGAAGGTTCTCAGCTAATT 300

QY 301 CTTGGCTAAGATGGGTTCCACATTAAGTCTGATAGTATGGGGGAAGGGTCAATTGGCT 360  
DB 301 CTTGGCTAAGATGGGTTCCACATTAAGTCTGATAGTATGGGGGAAGGGTCAATTGGCT 360

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGTCTTT 420  
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QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACACAAAGTCAC 480  
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QY 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAATCTACCGATTCACTTTAAGGCAGCA 540  
DB 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAATCTACCGATTCACTTTAAGGCAGCA 540

QY 541 GGACCAAGTTTGTAGTGGCAACATGAGCAGCAGAGATCAATGGAAACACAGATGATTGC 600  
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QY 601 AATGTCCTTTTTTTCTCTGCTCTGCTGACTTGATATAAAGGGGACCGT 647  
DB 601 AATGTCCTTTTTTTCTCTGCTCTGCTGACTTGATATAAAGGGGACCGT 647

RESULT 6  
LOCUS AR400152 647 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 308 from patent US 6620922.  
ACCESSION AR400152  
VERSION AR400152.1 GI:40143258  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 647)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6620922-A 308 16-SEP-2003;  
Corixa Corporation; Seattle, WA  
FEATURES  
source Location/Qualifiers  
1. .647  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 646; DB 2; Length 647;  
Best Local Similarity 100.0%; Pred. No. 7.6e-202; Indels 0; Gaps 0;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60  
DB 1 ACGATTTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

QY 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120  
DB 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120

QY 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTCTG 180  
DB 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACTGATCTCTTCTG 180

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240  
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

QY 241 CTAGAGAAAAGACCAACACCGGCTCAAGGATCTTTACCATGAAGGTTCTCAGCTAATT 300  
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QY 301 CTTGGCTAAGATGGGTTCCACATTAAGTCTGATAGTATGGGGGAAGGGTCAATTGGCT 360  
DB 301 CTTGGCTAAGATGGGTTCCACATTAAGTCTGATAGTATGGGGGAAGGGTCAATTGGCT 360

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGTCTTT 420  
DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCGGGGCTGCTTGTCTTT 420

QY 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACACAAAGTCAC 480  
DB 421 GGGAAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACACAAAGTCAC 480

QY 481 TGTATCAATTGCCATGAAGCTTGAGGACCTGAATCTACCGATTCACTTTAAGGCAGCA 540  
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QY 541 GGACCAAGTTTGTAGTGGCAACATGAGCAGCAGAGATCAATGGAAACACAGATGATTGC 600  
DB 541 GGACCAAGTTTGTAGTGGCAACATGAGCAGCAGAGATCAATGGAAACACAGATGATTGC 600

QY 601 AATGTCCTTTTTTTCTCTGCTCTGCTGACTTGATATAAAGGGGACCGT 647  
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RESULT 7  
LOCUS AR405419 647 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 308 from patent US 6630305.  
ACCESSION AR405419  
VERSION AR405419.1 GI:40154256  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 647)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6630305-A 308 07-OCT-2003;  
Corixa Corporation; Seattle, WA;  
WOX;  
FEATURES  
source Location/Qualifiers  
1. .647  
/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 646; DB 2; Length 647;  
Best Local Similarity 100.0%; Pred. No. 7,6e-202;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60  
DB 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60

QY 61 TGCCTCAGGGGAAGGTTCCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGATATAA 120  
DB 61 TGCCTCAGGGGAAGGTTCCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGATATAA 120

QY 121 GNGCCCTCAGATATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180  
DB 121 GNGCCCTCAGATATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAAGCCTACCTAATATCTG 240  
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAAGCCTACCTAATATCTG 240

QY 241 CTAGAGAAAGAACCAACACGGCCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300  
DB 241 CTAGAGAAAGAACCAACACGGCCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300

QY 301 CTTGGCTAGATCTGGGTTCCACATTAAGTTCGAAATATGGGGGAAGGTCATTTGCT 360  
DB 301 CTTGGCTAGATCTGGGTTCCACATTAAGTTCGAAATATGGGGGAAGGTCATTTGCT 360

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420  
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QY 421 GGAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACATCAAGTCTAC 480  
DB 421 GGAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACATCAAGTCTAC 480

QY 481 TGTATCAATTTGATGAGCTTTGAGGACCTGAATCTACCGATTCTTAAAGGAGCA 540  
DB 481 TGTATCAATTTGATGAGCTTTGAGGACCTGAATCTACCGATTCTTAAAGGAGCA 540

QY 541 GGACCAAGTTTGAAGTGGCAACAAATGAGCAGCAGCAGAGATCAATGGAACACAGATATTC 600  
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QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGACCGT 647  
DB 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGACCGT 647

RESULT 8

AR439623  
LOCUS  
DEFINITION  
SEQUENCE 308 from patent US 6664377.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AR439623  
Sequence 308 from patent US 6664377.  
AR439623.1 GI:42665532  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 647)  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Xu, J.  
Compounds for immunotherapy of prostate cancer and methods for their use  
Patent: US 6664377-A 308 16-DEC-2003;  
Corixa Corporation; Seattle, WA;  
WOX;  
Location/Qualifiers  
1. .647  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 646; DB 2; Length 647;  
Best Local Similarity 100.0%; Pred. No. 7,6e-202;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60  
DB 1 ACGATTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACACACAGCTGGAGCCAC 60

QY 61 TGCCTCAGGGGAAGGTTCCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGATATAA 120  
DB 61 TGCCTCAGGGGAAGGTTCCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGATATAA 120

QY 121 GNGCCCTCAGATATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180  
DB 121 GNGCCCTCAGATATAGATCTGTAGCAAGAAAGAAAGAAACAAACACTGATCTCTTCTG 180

QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAAGCCTACCTAATATCTG 240  
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAAGCCTACCTAATATCTG 240

QY 241 CTAGAGAAAGAACCAACACGGCCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300  
DB 241 CTAGAGAAAGAACCAACACGGCCTCAAGGATCTCTTACCATGAAGGTTCTCAGCTAAAT 300

QY 301 CTTGGCTAGATCTGGGTTCCACATTAAGTTCGAAATATGGGGGAAGGTCATTTGCT 360  
DB 301 CTTGGCTAGATCTGGGTTCCACATTAAGTTCGAAATATGGGGGAAGGTCATTTGCT 360

QY 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420  
DB 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTCTTT 420

QY 421 GGAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACATCAAGTCTAC 480  
DB 421 GGAACAATGGCTGAGCATATAACCATAGGTTATGGGAAACAAACATCAAGTCTAC 480

QY 481 TGTATCAATTTGATGAGCTTTGAGGACCTGAATCTACCGATTCTTAAAGGAGCA 540  
DB 481 TGTATCAATTTGATGAGCTTTGAGGACCTGAATCTACCGATTCTTAAAGGAGCA 540

QY 541 GGACCAAGTTTGAAGTGGCAACAAATGAGCAGCAGCAGAGATCAATGGAACACAGATATTC 600  
DB 541 GGACCAAGTTTGAAGTGGCAACAAATGAGCAGCAGCAGAGATCAATGGAACACAGATATTC 600

QY 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGACCGT 647  
DB 601 AATGTCCTTTTTTTCTCTGCTTCTGACTTGATAAAAGGGACCGT 647

RESULT 9

AR563799  
LOCUS  
DEFINITION  
SEQUENCE 308 from patent US 6759515.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AR563799  
Sequence 308 from patent US 6759515.  
AR563799.1 GI:53978850  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 647)  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Panger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Hedrick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.  
Compositions and methods for the therapy and diagnosis of prostate cancer  
Patent: US 6759515-A 308 06-JUL-2004;  
Corixa Corporation; Seattle, WA  
Location/Qualifiers  
1. .647  
/organism="unknown"



ORIGIN		/mol_type="genomic DNA"	
Query Match		100.0%; Score 646; DB 2; Length 647;	
Best Local Similarity		100.0%; Pred. No. 7.6e-202;	
Matches 647; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ACGATTTTCAATATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC	60
Db	1	ACGATTTTCAATATCATGTAATCGGGTCACTCAAGGGGCCAACACACAGCTGGGAGCCAC	60
Qy	61	TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA	120
Db	61	TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA	120
Qy	121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACCTGATCTCTTTCTG	180
Db	121	GGNGCCTCACAGTATAGATCTGGTAGCAAGAGAGAAACAAACACCTGATCTCTTTCTG	180
Qy	181	CCACCCCTCGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACTAATATCTG	240
Db	181	CCACCCCTCGACCCCTTTGGAACTCTCTGACCCCTTTAGAACCAAGCCTACTAATATCTG	240
Qy	241	CTAGAGAAAGACCAACACCGCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT	300
Db	241	CTAGAGAAAGACCAACACCGCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT	300
Qy	301	CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGTAATATGGGGGAAGGGTCAATTGGCT	360
Db	301	CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGTAATATGGGGGAAGGGTCAATTGGCT	360
Qy	361	CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT	420
Db	361	CATTTTGTGTGGATAAAGTCAGATGCCAGGGGCCAGAGCGGGGCTGCTTGCTTT	420
Qy	421	GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCAC	480
Db	421	GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAACACATCAAGTCAC	480
Qy	481	TGTATCAATTGGCCATGAAGACTTTGAGGGACCTGGAATCTACCGATTTCATCTTAAAGCAGCA	540
Db	481	TGTATCAATTGGCCATGAAGACTTTGAGGGACCTGGAATCTACCGATTTCATCTTAAAGCAGCA	540
Qy	541	GGACAGTTTGTAGTGGCAACAATCAGCAGCAGAGATCAATGGAACAACAAGATGATTGC	600
Db	541	GGACAGTTTGTAGTGGCAACAATCAGCAGCAGAGATCAATGGAACAACAAGATGATTGC	600
Qy	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647
Db	601	AATGTCCTTTTTTCTCTGCTTCTGACTTGATATAAAGGGGACCGT	647

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AR605605		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
LOCUS		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
DEFINITION		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
ACCESSION		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
VERSION		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
KEYWORDS		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
SOURCE		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
ORGANISM		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
REFERENCE		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
AUTHORS		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
TITLE		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
JOURNAL		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
FEATURES		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
source		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
1 (bases 1 to 647)		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
XU, J., DILLON, D. C., MITCHAM, J. L., HARLOCKER, S. L., JIANG, Y., KALOS, M. D., FANGER, G. R., RETTER, M. W., STOLK, J. A., DAY, C. H., VEDVICK, T. S., CARTER, D., LI, S. X., WANG, A., SKEIKY, Y. A. W., HEPLER, W. T. and HENDERSON, R. A.		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
Compositions and methods for the therapy and diagnosis of prostate cancer		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
Patent: US 680746-A 308 05-OCT-2004;		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
Corixa Corporation; Seattle, WA		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
Location/Qualifiers		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	
1 . 647		Sequence 308 from patent US 6818751.		AR605605		AR605605.1		GI:56657269	

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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 646; DB 2; Length 647;  
Best Local Similarity 100.0%; Pred. No. 7.6e-202;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATATCATGTAATCGGGTCACTCAAGGGGCCCAACACACAGCTGGGGCCAC 60  
DB 1 ACGATTTTCATATCATGTAATCGGGTCACTCAAGGGGCCCAACACACAGCTGGGGCCAC 60

QY 61 TGTCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120  
DB 61 TGTCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120

QY 121 GNGGCTCAGATATAGATCTGGTAGCAAGAGAAAGAAACAAACACTGATCTCTTTCTG 180  
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DEFINITION Sequence 308 from patent US 6894146.  
ACCESSION AR656944  
VERSION AR656944.1 GI:67590056  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 647)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T., and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6894146-A 308 17-MAY-2005; Corixa Corporation; Seattle, WA

Location/Qualifiers  
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/mol\_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 7.6e-202;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 308 from patent US 6943236.  
ACCESSION AR716851  
VERSION AR716851.1 GI:77365500  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 647)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T., Henderson,R.A., Hural,J., McNeill,P.D., Houghton,R.L., Vinals,Y. de Bassols,C., Foy,T.M., Watanabe,Y. and Meagher,M.J.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6943236-A 308 13-SEP-2005;

Corixa Corporation; Seattle, WA

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source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.6e-202;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 14

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LOCUS AX106197 647 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 335 from Patent WO0125273.

ACCESSION AX106197

VERSION AX106197.1 GI:13921887

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1

Skeiky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.

Compositions and methods for wt1 specific immunotherapy

Patent: WO 0125273-A 335 12-APR-2001;

JOURNAL

CORIXA CORPORATION (US)

Location/Qualifiers

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/mol\_type="unassigned DNA"  
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misc\_feature 1. .647  
/note="n = A,T,C or G"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.6e-202;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DEFINITION Sequence 308 from Patent WO0125272.

ACCESSION AX106527

VERSION AX106527.1 GI:13922205

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1

Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.

AUTHORS

REFERENCE

TITLE Compositions and methods for therapy and diagnosis of prostate

cancer

JOURNAL Patent: WO 0125272-A 308 12-APR-2001;

CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

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/note="n = A,T,C or G"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3	646	100.0	647	3	US-09-232-149A-308	Sequence 308, App
4	646	100.0	647	3	US-09-636-215-308	Sequence 308, App
5	646	100.0	647	3	US-09-685-166A-308	Sequence 308, App
6	646	100.0	647	3	US-09-688-489-308	Sequence 308, App
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11	646	100.0	647	3	US-10-012-896-308	Sequence 308, App
12	646	100.0	647	5	US-10-144-678A-308	Sequence 308, App
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## RESULT 2

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; Sequence 308, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-308
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Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
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; OTHER INFORMATION: n = A,T,C or G
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DB 61 TCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120
QY 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAAAGAAACAAACACCTGATCTCTTTCTG 180
DB 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAAAGAAACAAACACCTGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGGCTTAAATATCTG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGGCTTAAATATCTG 240
QY 241 CTAGAGAAAAGACCAACACGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
DB 241 CTAGAGAAAAGACCAACACGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
QY 301 CTTGGCTTAAGATGTGGTTTCCATTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
DB 301 CTTGGCTTAAGATGTGGTTTCCATTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 420
DB 361 CATTTTGTGTGGATAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAAACCATTAGGTTATGGGGAACAAACAAACATCAAGTCA 480
DB 421 GGGAAACAATGGCTGAGCATATAAACCATTAGGTTATGGGGAACAAACAAACATCAAGTCA 480
QY 481 TGTATCAATTTGCTGAGTAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 540
DB 481 TGTATCAATTTGCTGAGTAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 540
QY 541 GACCCAGTTTGAAGTGGCAACAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 600
DB 541 GACCCAGTTTGAAGTGGCAACAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 600
QY 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
DB 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647

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RESULT 5
US-09-685-166A-308
; Sequence 308, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien

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;
; NAME/KEY: misc feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-308

Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGATTTTCATTATCATGCTAATCGGTGCTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
DB 1 ACGATTTTCATTATCATGCTAATCGGTGCTCACTCAAGGGGCCCAACACAGCTGGGAGCCAC 60
QY 61 TCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120
DB 61 TCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCCAAGGTTCTATACAGGATATAAA 120
QY 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAAAGAAACAAACACCTGATCTCTTTCTG 180
DB 121 GNGCCTCACAGTATAGATCTGGTAGCAAGAGAAAGAAACAAACACCTGATCTCTTTCTG 180
QY 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGGCTTAAATATCTG 240
DB 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGGCTTAAATATCTG 240
QY 241 CTAGAGAAAAGACCAACACGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
DB 241 CTAGAGAAAAGACCAACACGCGCTCAAGAGGATCTCTTACCATGAAGGCTCAGCTAAT 300
QY 301 CTTGGCTTAAGATGTGGTTTCCATTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
DB 301 CTTGGCTTAAGATGTGGTTTCCATTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
QY 361 CATTTTGTGTGGATAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 420
DB 361 CATTTTGTGTGGATAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 420
QY 421 GGGAAACAATGGCTGAGCATATAAACCATTAGGTTATGGGGAACAAACAAACATCAAGTCA 480
DB 421 GGGAAACAATGGCTGAGCATATAAACCATTAGGTTATGGGGAACAAACAAACATCAAGTCA 480
QY 481 TGTATCAATTTGCTGAGTAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 540
DB 481 TGTATCAATTTGCTGAGTAAAGTCAGATGCCCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 540
QY 541 GACCCAGTTTGAAGTGGCAACAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 600
DB 541 GACCCAGTTTGAAGTGGCAACAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 600
QY 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
DB 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647

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RESULT 5
US-09-685-166A-308
; Sequence 308, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick

```

```
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-166A-308
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Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGGAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGGAAGAAACAAACACTGATCTCTTTCTG 180

Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
Db 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300

Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420

Qy 421 GGGAAACAATGGCTGAGCATATAACATAGTTTATGGGGAACAAACAAACATCAAAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACATAGTTTATGGGGAACAAACAAACATCAAAAGTCAC 480

Qy 481 TGTATCAATTGGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540
Db 481 TGTATCAATTGGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540

Qy 541 GGACAGGTTTGAGTGCGCAACAATGACGAGCAGAGATCAATGGAACACACAGATGATTGC 600
Db 541 GGACAGGTTTGAGTGCGCAACAATGACGAGCAGAGATCAATGGAACACACAGATGATTGC 600

Qy 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
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RESULT 6  
US-09-688-489-308  
; Sequence 308, Application US/09688489

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; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-688-489-308
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Query Match 100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60
Db 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60

Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
Db 61 TGCTCAGGGGAAGGTTTCATATGGGACTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120

Qy 121 GNGCCTCACAGTATAGATCTGGTAGCAAGGAAGAAACAAACACTGATCTCTTTCTG 180
Db 121 GNGCCTCACAGTATAGATCTGGTAGCAAGGAAGAAACAAACACTGATCTCTTTCTG 180

Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240
Db 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAACAGCCCTACCTAATATCTG 240

Qy 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
Db 241 CTAGAGAAAGACCAACACAGCCCTCAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300

Qy 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360
Db 301 CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTGCT 360

Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420
Db 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGGCTGCTTGCTTT 420

Qy 421 GGGAAACAATGGCTGAGCATATAACATAGTTTATGGGGAACAAACAAACATCAAAAGTCAC 480
Db 421 GGGAAACAATGGCTGAGCATATAACATAGTTTATGGGGAACAAACAAACATCAAAAGTCAC 480

Qy 481 TGTATCAATTGGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540
Db 481 TGTATCAATTGGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCAATCTTAAGGCAGCA 540

Qy 541 GGACAGGTTTGAGTGCGCAACAATGACGAGCAGAGATCAATGGAACACACAGATGATTGC 600
Db 541 GGACAGGTTTGAGTGCGCAACAATGACGAGCAGAGATCAATGGAACACACAGATGATTGC 600

Qy 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
Db 601 AATGTCCTTTTTTTTCTCTGCTTCTGACTTGTATAAAAGGGGACCGT 647
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RESULT 7  
US-09-679-426-308





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; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C or G
US-09-657-279-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 60
DB 1 ACAGTTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 60

QY 61 TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB 61 TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120

QY 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 180
DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 180

QY 181 CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
DB 181 CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240

QY 241 CTAGAGAAAGACCAACACAGGCTCTTACCAATGAAGGTTCTACAGTAAAT 300
DB 241 CTAGAGAAAGACCAACACAGGCTCTTACCAATGAAGGTTCTACAGTAAAT 300

QY 301 CTTGGCTAAGATGTGGGTTCCAACTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
DB 301 CTTGGCTAAGATGTGGGTTCCAACTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360

QY 361 CATTTTGTGTGGTAAAGTACAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420
DB 361 CATTTTGTGTGGTAAAGTACAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420

QY 421 GGAACAATGGCTGAGCATATACCATAGGTTATGGGGGAACAAACAACTCAAGTCTAC 480
DB 421 GGAACAATGGCTGAGCATATACCATAGGTTATGGGGGAACAAACAACTCAAGTCTAC 480

QY 481 TGTATCAATTTGCCATGAAGCTTTGAGGACCTGAATCTACCGATTCACTTAAGGAGCA 540
DB 481 TGTATCAATTTGCCATGAAGCTTTGAGGACCTGAATCTACCGATTCACTTAAGGAGCA 540

QY 541 GACACAGTTTGTAGTGGCAACATGCAGCAGCAGATCAATGGAACAAACAGATGATTCG 600
DB 541 GACACAGTTTGTAGTGGCAACATGCAGCAGCAGATCAATGGAACAAACAGATGATTCG 600

QY 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
DB 601 AATGTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 647
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## RESULT 11

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US-10-012-896-308
; Sequence 308, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
```

```
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-308

Query Match      100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 60
DB 1 ACAGTTTTCATTATCATGTAAATCGGTCACTCAAGGGGCCCAACACAGCTGGAGCCAC 60

QY 61 TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120
DB 61 TGTCTAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120

QY 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 180
DB 121 GNGGCTTCACAGTATAGATCTGTAGCAAGAGAGAAACAACTGATCTCTTTCTG 180

QY 181 CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240
DB 181 CCACCCCTCTGACCTTTTGGAACTCTCTGACCTTTAGAACAGGCTACCTAATATCTG 240

QY 241 CTAGAGAAAGACCAACACAGGCTCTTACCAATGAAGGTTCTACAGTAAAT 300
DB 241 CTAGAGAAAGACCAACACAGGCTCTTACCAATGAAGGTTCTACAGTAAAT 300

QY 301 CTTGGCTAAGATGTGGGTTCCAACTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360
DB 301 CTTGGCTAAGATGTGGGTTCCAACTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360

QY 361 CATTTTGTGTGGTAAAGTACAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420
DB 361 CATTTTGTGTGGTAAAGTACAGATGCCAGGGGCCAGAGCAGGGGGCTGCTCTCTTT 420

QY 421 GGAACAATGGCTGAGCATATACCATAGGTTATGGGGGAACAAACAACTCAAGTCTAC 480
DB 421 GGAACAATGGCTGAGCATATACCATAGGTTATGGGGGAACAAACAACTCAAGTCTAC 480

QY 481 TGTATCAATTTGCCATGAAGCTTTGAGGACCTGAATCTACCGATTCACTTAAGGAGCA 540
DB 481 TGTATCAATTTGCCATGAAGCTTTGAGGACCTGAATCTACCGATTCACTTAAGGAGCA 540

QY 541 GACACAGTTTGTAGTGGCAACATGCAGCAGCAGATCAATGGAACAAACAGATGATTCG 600
DB 541 GACACAGTTTGTAGTGGCAACATGCAGCAGCAGATCAATGGAACAAACAGATGATTCG 600
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Db 696 TGCTCAGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 755  
Qy 121 GGGGCTCAGATATAGATCTGGTAGCAAGAGAGAGAACCAACACATGATCTCTTTCTG 180  
Db 756 GGTGCTCAGATATAGATCTGGTAGCAAGAGAGAGAACCAACACATGATCTCTTTCTG 815  
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAGCCTACCTAATATCTG 240  
Db 816 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAGCCTACCTAATATCTG 875  
Qy 241 CTAGAGAAAAGCAACCAACCGGCTTCAAGAGATCTCTTACCATGAAGGTTCTCAGCTAAT 300  
Db 876 CTAGAGAAAAGCAACCAACCGGCTTCAAGAGATCTCTTACCATGAAGGTTCTCAGCTAAT 935  
Qy 301 CTTGGCTAAGATGTGGTTCCACATTTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360  
Db 936 CTTGGCTAAGATGTGGTTCCACATTTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 995  
Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 420  
Db 996 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 1054  
Qy 421 GGGAAACAATGGCTGAGCATATACCATAGGTTTATGGGGAACAAAACAACATCAAAAGTCAC 480  
Db 1055 GGGAAACAATGGCTGAGCATATACCATAGGTTTATGGGGAACAAAACAACATCAAAAGTCAC 1111  
Qy 481 TGTATCAATTTGAGTGCAACAATGACGAGCAGAGATCAATGGAACAACAGATGATTCG 600  
Db 1112 TGTATCAATTTGAGTGCAACAATGACGAGCAGAGATCAATGGAACAACAGATGATTCG 1231  
Qy 601 AATGTCCTTTTTTTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641  
Db 1232 AATGTCCTTTTTTTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272

## RESULT 14

US-09-685-166A-552  
; Sequence 552, Application US/09685166A  
; Patent No. 6630305

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrik  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William

## TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C21

CURRENT APPLICATION NUMBER: US/09/685,166A

CURRENT FILING DATE: 2000-10-10

NUMBER OF SEQ ID NOS: 898

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 552

LENGTH: 2577

TYPE: DNA

ORGANISM: Homo sapiens

## US-09-685-166A-552

Query Match 92.8%; Score 599.2; DB 3; Length 2577;

Best Local Similarity 98.0%; Pred. No. 2.6e-190;

Matches 628; Conservative 0; Mismatches 9; Indels 4; Gaps 2;

Qy 1 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 60  
Db 636 ACGATTTTCATTATCATGTAAATCGGGTCACCTCAAGGGGCCAACACACAGCTGGGAGCCAC 695  
Qy 61 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 120  
Db 696 TGCTCAGGGGAAGGTTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAA 755  
Qy 121 GGGGCTCAGATATAGATCTGGTAGCAAGAGAGAGAACCAACACATGATCTCTTTCTG 180  
Db 756 GGTGCTCAGATATAGATCTGGTAGCAAGAGAGAGAACCAACACATGATCTCTTTCTG 815  
Qy 181 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAGCCTACCTAATATCTG 240  
Db 816 CCACCCCTCTGACCCCTTTGGAACTCTCTGACCCCTTTAGAAACAAGCCTACCTAATATCTG 875  
Qy 241 CTAGAGAAAAGCAACCAACCGGCTTCAAGAGATCTCTTACCATGAAGGTTCTCAGCTAAT 300  
Db 876 CTAGAGAAAAGCAACCAACCGGCTTCAAGAGATCTCTTACCATGAAGGTTCTCAGCTAAT 935  
Qy 301 CTTGGCTAAGATGTGGTTCCACATTTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 360  
Db 936 CTTGGCTAAGATGTGGTTCCACATTTAGGTTCTGAATATGGGGGAAGGTTCAATTTGCT 995  
Qy 361 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 420  
Db 996 CATTTTGTGTGGATAAAGTCAGGATGCCAGGGGCCAGAGCAGGGGCTGCTTTGCTTT 1054  
Qy 421 GGGAAACAATGGCTGAGCATATACCATAGGTTTATGGGGAACAAAACAACATCAAAAGTCAC 480  
Db 1055 GGGAAACAATGGCTGAGCATATACCATAGGTTTATGGGGAACAAAACAACATCAAAAGTCAC 1111  
Qy 481 TGTATCAATTTGAGTGCAACAATGACGAGCAGAGATCAATGGAACAACAGATGATTCG 540  
Db 1112 TGTATCAATTTGAGTGCAACAATGACGAGCAGAGATCAATGGAACAACAGATGATTCG 1171  
Qy 541 GGACCAAGTTTGGTGCAACAATGACGAGCAGAGATCAATGGAACAACAGATGATTCG 600  
Db 1172 GGACCAAGTTTGGTGCAACAATGACGAGCAGAGATCAATGGAACAACAGATGATTCG 1231  
Qy 601 AATGTCCTTTTTTTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641  
Db 1232 AATGTCCTTTTTTTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272

## RESULT 15

US-09-679-426-552

; Sequence 552, Application US/09679426

; Patent No. 6759515

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrik  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William





GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:18:37 ; Search time 122.772 Seconds  
(without alignments)  
8016.516 Million cell updates/sec

Title: US-09-232-880-311

Perfect score: 525

Sequence: 1 caaatattgagccaatgacat.....tttaatcccaagcacagt 526

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/ina/H COMB.seq:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq:\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq:\*
- 9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq:\*
- 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	100.0	526	3	US-09-439-313-311 Sequence 311, App
2	525	100.0	526	3	US-09-352-616A-311 Sequence 311, App
3	525	100.0	526	3	US-09-232-149A-311 Sequence 311, App
4	525	100.0	526	3	US-09-636-215-311 Sequence 311, App
5	525	100.0	526	3	US-09-685-166A-311 Sequence 311, App
6	525	100.0	526	3	US-09-688-489-311 Sequence 311, App
7	525	100.0	526	3	US-09-679-426-311 Sequence 311, App
8	525	100.0	526	3	US-09-759-143-311 Sequence 311, App
9	525	100.0	526	3	US-09-651-236-311 Sequence 311, App
10	525	100.0	526	3	US-09-657-279-311 Sequence 311, App
11	525	100.0	526	3	US-10-012-896-311 Sequence 311, App
12	525	100.0	526	5	US-10-144-678A-311 Sequence 311, App
C 13	469.2	89.4	3434	3	US-09-439-313-476 Sequence 476, App
C 14	469.2	89.4	3434	3	US-09-636-215-476 Sequence 476, App
C 15	469.2	89.4	3434	3	US-09-685-166A-476 Sequence 476, App
C 16	469.2	89.4	3434	3	US-09-679-426-476 Sequence 476, App
C 17	469.2	89.4	3434	3	US-09-759-143-476 Sequence 476, App
C 18	469.2	89.4	3434	3	US-09-651-236-476 Sequence 476, App
C 19	469.2	89.4	3434	3	US-09-657-279-476 Sequence 476, App
C 20	469.2	89.4	3434	3	US-10-012-896-476 Sequence 476, App
C 21	469.2	89.4	3434	5	US-10-144-678A-476 Sequence 476, App
C 22	261.6	49.8	2414	3	US-09-439-313-475 Sequence 475, App
C 23	261.6	49.8	2414	3	US-09-636-215-475 Sequence 475, App

C 24	261.6	49.8	2414	3	US-09-685-166A-475	Sequence 475, App
C 25	261.6	49.8	2414	3	US-09-679-426-475	Sequence 475, App
C 26	261.6	49.8	2414	3	US-09-759-143-475	Sequence 475, App
C 27	261.6	49.8	2414	3	US-09-651-236-475	Sequence 475, App
C 28	261.6	49.8	2414	3	US-09-657-279-475	Sequence 475, App
C 29	261.6	49.8	2414	3	US-10-012-896-475	Sequence 475, App
C 30	261.6	49.8	2414	5	US-10-144-678A-475	Sequence 475, App
C 31	109	20.8	1594	3	US-09-439-313-474	Sequence 474, App
C 32	109	20.8	1594	3	US-09-636-215-474	Sequence 474, App
C 33	109	20.8	1594	3	US-09-685-166A-474	Sequence 474, App
C 34	109	20.8	1594	3	US-09-679-426-474	Sequence 474, App
C 35	109	20.8	1594	3	US-09-759-143-474	Sequence 474, App
C 36	109	20.8	1594	3	US-09-651-236-474	Sequence 474, App
C 37	109	20.8	1594	3	US-09-657-279-474	Sequence 474, App
C 38	109	20.8	1594	3	US-10-012-896-474	Sequence 474, App
C 39	109	20.8	1594	5	US-10-144-678A-474	Sequence 474, App
C 40	43.2	8.2	317366	3	US-09-949-016-16001	Sequence 16001, A
C 41	42.2	8.1	101674	3	US-09-949-016-12033	Sequence 12033, A
C 42	42.2	8.0	50000	3	US-09-662-254B-26	Sequence 26, Appli
C 43	42	8.0	1664976	3	US-08-916-421B-1	Sequence 1, Appli
C 44	42	8.0	1664976	3	US-09-692-570-1	Sequence 1, Appli
C 45	41.8	8.0	109925	3	US-09-949-016-13210	Sequence 13210, A

#### ALIGNMENTS

RESULT 1  
US-09-439-313-311  
; Sequence 311, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqi  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 311  
; LENGTH: 526  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(526)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-439-313-311

Query Match 100.0%; Score 525; DB 3; Length 526;

Best Local Similarity 100.0%; Pred. No. 9.5e-125; Mismatches 0; Indels 0; Gaps 0; Matches 526; Conservative 0;

QY 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 60

Db 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 60

QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCCAATAATATATATCTA 120

Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCCAATAATATATATCTA 120

QY 121 CATTTCACGATTTTAAATATGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

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Db 121 CATTTACAGCAATTTAAATGTTTTCAGCATGAAATATTAGTACAGGGGAAGCTTAATAA 180
Qy 181 ATTAACAATGGAATAAGATTGTCTTAAATATAATCTACAAGAAGCTTTGATATTG 240
Db 181 ATTAACAATGGAATAAGATTGTCTTAAATATAATCTACAAGAAGCTTTGATATTG 240
Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTTACAGACTCCATAACC 360
Db 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGCTCTCTGAGCCCTCAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCTCTGAGCCCTCAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480
Qy 481 AGTTCTATAAAGTGTAGTACTTATTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGTGTAGTACTTATTTTAAATCCCAAGCACAGT 526
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## RESULT 2

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US-09-352-616A-311
; Sequence 311, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yucui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-311
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Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120
Db 61 TTTTGACGTTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120

Qy 121 CATTTACAGCAATTTAAATGTTTTCAGCATGAAATATTAGTCTACAAGGAAGCTTAATAA 180
Db 121 CATTTACAGCAATTTAAATGTTTTCAGCATGAAATATTAGTCTACAAGGAAGCTTAATAA 180

Qy 181 ATTAACAATGGAATAAGATTGTCTTAAATATAATCTACAAGAAGCTTTGATATTG 240
Db 181 ATTAACAATGGAATAAGATTGTCTTAAATATAATCTACAAGAAGCTTTGATATTG 240
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Db 181 ATTAACAATGGAATAAGATTGTCTTAAATATAATCTACAAGAAGCTTTGATATTG 240
Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTTACAGACTCCATAACC 360
Db 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGCTCTCTGAGCCCTCAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCTCTGAGCCCTCAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAA 480
Qy 481 AGTTCTATAAAGTGTAGTACTTATTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGTGTAGTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 3
US-09-232-149A-311
; Sequence 311, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-311
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Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Qy 61 TTTTGAGCTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120
Db 61 TTTTGAGCTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATTATATCTA 120

Qy 121 CATTTACAGCAATTTAAATGTTTTCAGCATGAAATATTAGTCTACAAGGAAGCTTAATAA 180
Db 121 CATTTACAGCAATTTAAATGTTTTCAGCATGAAATATTAGTCTACAAGGAAGCTTAATAA 180

Qy 181 ATTAACAATGGAATAAGATTGTCTTAAATATAATCTACAAGAAGCTTTGATATTG 240
Db 181 ATTAACAATGGAATAAGATTGTCTTAAATATAATCTACAAGAAGCTTTGATATTG 240

Qy 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 241 TTTTTCACAAGTGAAGCAATCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Qy 301 AAAATGGGGAAGCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTTACAGACTCCATAACC 360
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Db 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAAA 480  
QY 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526  
Db 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526

## RESULT 4

US-09-636-215-311  
; Sequence 311, Application US/09636215  
; Patent No. 6620922

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215  
; CURRENT FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 852  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 311  
; LENGTH: 526  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(526)  
; OTHER INFORMATION: n = A,T,C or G

## US-09-636-215-311

Query Match 100.0%; Score 525; DB 3; Length 526;  
Best Local Similarity 100.0%; Pred. No. 9.5e-125;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAATCAAGAAGCTTATCTGGGGCCATTTC 60  
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAATCAAGAAGCTTATCTGGGGCCATTTC 60  
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATATCTA 120  
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATATCTA 120  
QY 121 CATTTACAGATTTAAATGCTTTTCAGCATGAATATTAGCTACAGGGAGCTAAATAA 180  
Db 121 CATTTACAGATTTAAATGCTTTTCAGCATGAATATTAGCTACAGGGAGCTAAATAA 180  
QY 181 ATTAACATCGGAATAAAGATTTCTCCTTAAATATAATCTACAAGAGACCTTTTGATATTG 240

Db 181 ATTAACATCGGAATAAAGATTTCTCCTTAAATATAATCTACAAGAGACCTTTTGATATTG 240  
QY 241 TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCAAACTTTTGGGGAAACTATCGGAA 300  
Db 241 TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCAAACTTTTGGGGAAACTATCGGAA 300  
QY 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTAACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTAACCTGAAGCTACAGACTCCATAACC 360  
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAAAGTATCTGTGTATCAAGTATAAA 480  
QY 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526  
Db 481 AGTTCTATAAAGCTGTAGTNTACTTTTAAATCCCAAGCACAGT 526

## RESULT 5

US-09-685-166A-311  
; Sequence 311, Application US/09685166A  
; Patent No. 6630305

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C21  
; CURRENT APPLICATION NUMBER: US/09/685,166A  
; CURRENT FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 898  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 311  
; LENGTH: 526  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(526)  
; OTHER INFORMATION: n = A,T,C or G

## US-09-685-166A-311

Query Match 100.0%; Score 525; DB 3; Length 526;  
Best Local Similarity 100.0%; Pred. No. 9.5e-125;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAATCAAGAAGCTTATCTGGGGCCATTTC 60  
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAATCAAGAAGCTTATCTGGGGCCATTTC 60  
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATATCTA 120  
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATATCTA 120

QY	121	CATTTTACAGCATTTTAAATGTGTT	CAGCATGAAATATTAGCTACAGGGGAGCTAAATAA	180
DB	121	CATTTTACAGCATTTTAAATGTGTT	CAGCATGAAATATTAGCTACAGGGGAGCTAAATAA	180
QY	181	ATTAAACATGGGAATAAAGATTGT	CTCTTAAATATAAATCTACAAGAAGACTTTGATATTTG	240
DB	181	ATTAAACATGGGAATAAAGATTGT	CTCTTAAATATAAATCTACAAGAAGACTTTGATATTTG	240
QY	241	TTTTTCACAAGTGAAGCATTTCTTA	TAAAGTGTCAATAACCTTTTGGGGAAACCTATCGGAA	300
DB	241	TTTTTCACAAGTGAAGCATTTCTTA	TAAAGTGTCAATAACCTTTTGGGGAAACCTATCGGAA	300
QY	301	AAAATGGGGAAACTCTGAAGGGTT	TAAAGTATCTTACCTGAAGCTACAGACTCCATAACC	360
DB	301	AAAATGGGGAAACTCTGAAGGGTT	TAAAGTATCTTACCTGAAGCTACAGACTCCATAACC	360
QY	361	TCCTCTTTACAGGGAGCTCCTG	CAGGCCCTCACAGAAATGAGTGGCTGAGATCTTTGATTCG	420
DB	361	TCCTCTTTACAGGGAGCTCCTG	CAGGCCCTCACAGAAATGAGTGGCTGAGATCTTTGATTCG	420
QY	421	ACAGCAAGAGCTTCTCATCTAAAC	CCCTTTCCTTTTAGTATCTGTGATCAAGTATAAA	480
DB	421	ACAGCAAGAGCTTCTCATCTAAAC	CCCTTTCCTTTTAGTATCTGTGATCAAGTATAAA	480
QY	481	AGTCTTATAAATCTGTAGTNWTA	CTTATTTTAAATCCCCAAAGCACAGT	526
DB	481	AGTCTTATAAATCTGTAGTNWTA	CTTATTTTAAATCCCCAAAGCACAGT	526

## RESULT 6

RESOLUTION 8  
US-09-688-489-311  
: Sequence 311, Application US/09688489

Sequence 311, Application 05/05060403  
; Patent No. 6664377  
; GENERAL INFORMATION:

GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.

APPLICANT: Mitchem, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

FILE OF INVENTION: 210121.427D2  
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.427D2

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; FILE ADDRESS: 21001117.D
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13

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Query Match	Score 525;	DB 3;	Length 526;
Best Local Similarity	100.0%;		
Matches 526;	Conservative	0;	Indels 0;
	Mismatches	0;	Gaps 0;
	Pred. No.	9.5e-125;	

QY	61	TTTTGACGTTTTCTCTAAACTCTAAAGAGCGCATTAAATGATCCATAAAATTATATTATCTA	120
Dh	61	TTTTTGGACGTTTTCTCTAACTCTAAAGAGCGCATTAAATGATCCATAAAATTATATTATCTA	120

Qy	121	121	121	180
Qy	CA	TTTACAGCATTTTAAAAATGTT	CAGCATGAAATATTAGCTACAGGGGAAGCT	TAATAA
D <sub>b</sub>	121	CA	TTTACAGCATTTTAAAAATGTT	CAGCATGAAATATTAGCTACAGGGGAAGCT
D <sub>b</sub>	180	CA	TTTACAGCATTTTAAAAATGTT	CAGCATGAAATATTAGCTACAGGGGAAGCT

181 ATTAACATGGATAAAGATTTGTCTTAATATATCTACAAGAAGACTTTGATATTG 240

Db	181	ATTTAAACATGGAAATAAGATTGTGCTCTTAAATATAATCTCAAGAGAGACTTTTGATTTTG	240
Qy	241	TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCTATAACCTTTTTTGGGGAAACTATGGAA	300
Db	241	TTTTTCACAAGTGAAGCATTTCTTATAAAGTGTCTATAAACCCTTTTTTGGGGAAACTATGGAA	300
Qy	301	AAAATGGGGAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATACCC	360
Db	301	AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATACCC	360
Qy	361	TCTCTTTACAGGGAGCTCTCTGCAGCCCTCTACAGAAATGAGTGGCTGAGATTTCTTGATTC	420
Db	361	TCTCTTTACAGGGAGCTCTCTGCAGCCCTCTACAGAAATGAGTGGCTGAGATTTCTTGATTC	420
Qy	421	ACAGCAAGAGTCTCGATCTATAAGCCCTTCCCTTTTGTAGTATCTGTATCAAGTATATAA	480
Db	421	ACAGCAAGAGTCTCTCATCTATAAGCCCTTCCCTTTTGTAGTATCTGTATCAAGTATATAA	480
Qy	481	AGTTCTATAAAGCTAGTNTACTTTATTTTAAATCCCAAAGCACAGT	526
Db	481	AGTTCTATAAAGCTAGTNTACTTTATTTTAAATCCCAAAGCACAGT	526

## RESULT 7

US-09-679-426-311  
: Sequence 311. Application US/09679426

Sequence ID, Application 05/0507512  
Patent No. 6759515  
GENERAL INFORMATION:

Query Match	100.0%	Score 525;	DB 3;	Length 526;
Best Local Similarity	100.0%	Pred. No. 9.5e-125;		
Matches 526:	Conservative	0;	Mismatches 0;	Indels 0;
Gaps				0;

Qy	61	TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAAATTATATATCTA	120
Ph	61	TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAAATTATATATCTA	120

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QY 121 CATTTCAGCATTAAATGTTTACGATGAATATTAGCTACAGGGAGCTAAATAA 180
Db 121 CATTTCAGCATTAAATGTTTACGATGAATATTAGCTACAGGGAGCTAAATAA 180
QY 181 ATTAACATGGAATAAGATTGTCCTTAATAATAATCTACAAGAGACTTTGATATTG 240
Db 181 ATTAACATGGAATAAGATTGTCCTTAATAATAATCTACAAGAGACTTTGATATTG 240
QY 241 TTTTTCACAGTGAAGCTCTTATAAAGTGTCTAAACCTTTTGGGGAACCTATGGGA 300
Db 241 TTTTTCACAGTGAAGCTCTTATAAAGTGTCTAAACCTTTTGGGGAACCTATGGGA 300
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGTGATCTTGATTTG 420
Db 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGTGATCTTGATTTG 420
QY 421 ACAGCAGAGCTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 526
Db 421 ACAGCAGAGCTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 526
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## RESULT 8

US-09-759-143-311

; Sequence 311, Application US/09759143

; Patent No. 6800746

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 311

; LENGTH: 526

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(526)

; OTHER INFORMATION: n = A, T, C or G

US-09-759-143-311

Query Match

Best Local Similarity 100.0%; Score 525; DB 3; Length 526;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAAATTGAGCCAAATGACATAGAATTTTACAAATCAAGAGCTTATTTCTGGGSCATTTC 60
Db 1 CAAATTGAGCCAAATGACATAGAATTTTACAAATCAAGAGCTTATTTCTGGGSCATTTC 60
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATTATCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATTATCTA 120
QY 121 CATTTCACAGCTTTAAATGTTTACGATGAATATTAGCTACAGGGAGCTAAATAA 180
Db 121 CATTTCACAGCTTTAAATGTTTACGATGAATATTAGCTACAGGGAGCTAAATAA 180
QY 181 ATTAACATGGAATAAGATTGTCCTTAATAATAATCTACAAGAGACTTTGATATTG 240
Db 181 ATTAACATGGAATAAGATTGTCCTTAATAATAATCTACAAGAGACTTTGATATTG 240
QY 241 TTTTTCACAGTGAAGCTCTTATAAAGTGTCTAAACCTTTTGGGGAACCTATGGGA 300
Db 241 TTTTTCACAGTGAAGCTCTTATAAAGTGTCTAAACCTTTTGGGGAACCTATGGGA 300
QY 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
QY 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGTGATCTTGATTTG 420
Db 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGTGATCTTGATTTG 420
QY 421 ACAGCAGAGCTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 480
Db 421 ACAGCAGAGCTTCTCATCTAAACCTTTTAAATCCCAAGCACAGT 480
QY 481 AGTTCTATAAAGCTGTAGTNTACTTATTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTGTAGTNTACTTATTTAAATCCCAAGCACAGT 526
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## RESULT 9

US-09-651-236-311

; Sequence 311, Application US/09651236

; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 311

; LENGTH: 526

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(526)

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; OTHER INFORMATION: n = A,T,C or G
US-09-651-236-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATTCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATTCTA 120
Qy 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Qy 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATATCTACAAGAAGCTTTGATATTGG 240
Db 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATATCTACAAGAAGCTTTGATATTGG 240
Qy 241 TTTTTCACAGGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAACCTATGGAA 300
Db 241 TTTTTCACAGGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAACCTATGGAA 300
Qy 301 AAAATGGGAAACTCTGAAGGGTTTTTAAGTATCTTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAAACTCTGAAGGGTTTTTAAGTATCTTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
Db 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
Qy 481 AGTTCTATAAAGCTAGTNTACTTTATTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTAGTNTACTTTATTTTAAATCCCAAGCACAGT 526
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US-09-657-279-311
; Sequence 311, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-657-279-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATTCTA 120
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATTCTA 120
Qy 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Qy 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATATCTACAAGAAGCTTTGATATTGG 240
Db 181 ATTAACATGGAATAAAGATTTGTCTTAAATATATATCTACAAGAAGCTTTGATATTGG 240
Qy 241 TTTTTCACAGGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAACCTATGGAA 300
Db 241 TTTTTCACAGGTGAAGCAATCTTATAAAGTGTCAATAACCTTTTGGGGAACCTATGGAA 300
Qy 301 AAAATGGGAAACTCTGAAGGGTTTTTAAGTATCTTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGAAACTCTGAAGGGTTTTTAAGTATCTTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
Db 361 TCTCTTTACAGGAGGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAA 480
Qy 481 AGTTCTATAAAGCTAGTNTACTTTATTTTAAATCCCAAGCACAGT 526
Db 481 AGTTCTATAAAGCTAGTNTACTTTATTTTAAATCCCAAGCACAGT 526
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RESULT 11
US-10-012-896-311
; Sequence 311, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
```

```
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Basols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 499
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTGACCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
DB 1 CAAATTGACCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
DB 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120

QY 121 CATTTACAGCAATTTAAATGTTTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 180
DB 121 CATTTACAGCAATTTAAATGTTTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 180

QY 181 ATTTAAACATGGAATAAAGATTGTTCTTAAATATATCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 240
DB 181 ATTTAAACATGGAATAAAGATTGTTCTTAAATATATCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 240

QY 241 TTTTTCACAGTGAAGCAATCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAA 300
DB 241 TTTTTCACAGTGAAGCAATCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAA 300

QY 301 AAAATGGGAAAACCTCTGAAGGGTTTAAAGTATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 360
DB 301 AAAATGGGAAAACCTCTGAAGGGTTTAAAGTATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 360

QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGTGATTC 420
DB 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGTGATTC 420

QY 421 ACAGCAAGAGCTTCTCATCTAAACCCTTCCCTTTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 480
DB 421 ACAGCAAGAGCTTCTCATCTAAACCCTTCCCTTTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 480

QY 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAAATCCCAAGCAGT 526
DB 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAAATCCCAAGCAGT 526
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## RESULT 12

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US-10-144-678A-311
; Sequence 311, Application US/10144678A
; Patent No. 7033827
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

```
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Basols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 499
; OTHER INFORMATION: n = A,T,C or G
US-10-144-678A-311
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Query Match      100.0%; Score 525; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTGACCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
DB 1 CAAATTGACCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
DB 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120

QY 121 CATTTACAGCAATTTAAATGTTTCTTAAATATATCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 180
DB 121 CATTTACAGCAATTTAAATGTTTCTTAAATATATCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 180

QY 181 ATTTAAACATGGAATAAAGATTGTTCTTAAATATATCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 240
DB 181 ATTTAAACATGGAATAAAGATTGTTCTTAAATATATCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 240

QY 241 TTTTTCACAGTGAAGCAATCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAA 300
DB 241 TTTTTCACAGTGAAGCAATCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAAAGTCTTATAA 300

QY 301 AAAATGGGAAAACCTCTGAAGGGTTTAAAGTATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 360
DB 301 AAAATGGGAAAACCTCTGAAGGGTTTAAAGTATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 360

QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGTGATTC 420
DB 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGTGATTC 420

QY 421 ACAGCAAGAGCTTCTCATCTAAACCCTTCCCTTTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 480
DB 421 ACAGCAAGAGCTTCTCATCTAAACCCTTCCCTTTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 480
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:07:59 ; Search time 408.854 Seconds  
(without alignments)  
8969.963 Million cell updates/sec

Title: US-09-232-880-311

Perfect score: 525

Sequence: 1 caaataggagcaaatgacat.....tttaatcccaaacacagt 526

Scoring table: IDENTITY\_NUC

Gap 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:.\*  
3: Geneseqn2000s:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	525	100.0	526	4	AAH02724 Prostate
5	525	100.0	526	4	AAH84973 Human pro
6	525	100.0	526	4	AAH86941 Human P77
7	525	100.0	526	5	ACA59560 Prostate
8	525	100.0	526	6	ABL95123 Human P77
9	525	100.0	526	8	ACC95287 Prostate
10	525	100.0	526	10	ADB13761 Human pro
11	525	100.0	526	10	ADG26177 Human pro
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c 20	469.2	89.4	3434	4	AAH85125
c 21	469.2	89.4	3434	5	ACA59712
c 22	469.2	89.4	3434	6	ABL95275
c 23	469.2	89.4	3434	8	ACC95439
c 24	469.2	89.4	3434	10	ADB13926
c 25	469.2	89.4	3434	10	ADG26342
c 26	469.2	89.4	3434	15	AEF66623
c 27	387.4	73.8	473	5	ABV13051
c 28	372.4	70.9	492	5	ABV34172
c 29	330.4	62.9	453	5	ABV03882
c 30	265.8	50.6	2413	10	ADB75614
c 31	261.6	49.8	2414	4	AAH93810
c 32	261.6	49.8	2414	4	AA063903
c 33	261.6	49.8	2414	4	AAH85124
c 34	261.6	49.8	2414	5	ACA59711
c 35	261.6	49.8	2414	6	ABL95274
c 36	261.6	49.8	2414	8	ACC95438
c 37	261.6	49.8	2414	10	ADB13925
c 38	261.6	49.8	2414	10	ADG26341
c 39	261.6	49.8	2414	15	AEF66622
c 40	145.8	27.8	1723	6	ABD38814
c 41	109	20.8	1594	4	AAH93809
c 42	109	20.8	1594	4	AA063902
c 43	109	20.8	1594	4	AAH85123
c 44	109	20.8	1594	5	ACA59710
c 45	109	20.8	1594	6	ABL95273

## ALIGNMENTS

### RESULT 1

AAA06543

ID AAA06543 standard; cDNA; 526 BP.

XX

AC AAA06543;

XX

DT 13-JUN-2000 (first entry)

XX

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:311.

XX

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

KW immunogenic; cytostatic; vaccine; ss.

XX

OS Homo sapiens.

XX

PN WO200004149-A2.

XX

PD 27-JAN-2000.

XX

PF 14-JUL-1999; 99WO-US015838.

XX

PR 14-JUL-1998; 98US-00115453.

PR

PR 14-JUL-1998; 98US-00116134.

PR

PR 23-SEP-1998; 98US-00159812.

PR

PR 23-SEP-1998; 98US-00159822.

PR

PR 15-JAN-1999; 99US-00232149.

PR

PR 15-JAN-1999; 99US-00232880.

PR

PR 09-APR-1999; 99US-00288946.

XX

PA (CORI-) CORIXA CORP.

XX

PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;

XX

DR WPI; 2000-171268/15.

XX

PT New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein.

XX

PS Claim 1; Page 199; 263pp; English.

XX

CC The present invention describes isolated polypeptides, comprising an

CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides  
CC and polynucleotides encoding them have cytostatic activity and can be  
CC used in vaccines and in gene therapy. The polypeptides and  
CC polynucleotides encoding them, antigen presenting cells which express the  
CC polypeptides, antibodies against the polypeptides and vaccines comprising  
CC them can be used for inhibiting the development of prostate cancer in a  
CC patient. The polypeptides can be used to generate antibodies or anti-  
CC idotypic antibodies for passive immuno therapy. A portion of the  
CC polynucleotides encoding the polypeptides can be used as a probe or to  
CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and  
CC AAY82000 to AAY82020 represent sequences used in the exemplification of  
CC the present invention  
XX

SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 3; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTTC 60  
Db 1 CAAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTTC 60  
Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAATTATATATCTA 120  
Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAATTATATATCTA 120  
Qy 121 CATTTACAGCATTTAAATATGTTTCAGCATGAAATATTAGTCACAGGGGAAGCTTAAATAA 180  
Db 121 CATTTACAGCATTTAAATATGTTTCAGCATGAAATATTAGTCACAGGGGAAGCTTAAATAA 180  
Qy 181 ATTAACAATGGAATAAAGATTGTCCTTAAATATAATCTACAAGAAGCTTTGATATTTG 240  
Db 181 ATTAACAATGGAATAAAGATTGTCCTTAAATATAATCTACAAGAAGCTTTGATATTTG 240  
Qy 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300  
Db 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300  
Qy 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Qy 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAAA 480  
Qy 481 AGTTCTATAAATCTGAGTNTACTTATTTTAAATCCCAAGACACAGT 526  
Db 481 AGTTCTATAAATCTGAGTNTACTTATTTTAAATCCCAAGACACAGT 526

RESULT 2  
ID AAH93659  
XX AAH93659 standard; cDNA; 526 BP.  
XX AC AAH93659;

XX 04-OCT-2001 (first entry)  
XX Human prostate-specific cDNA sequence P775P.  
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
XX cytostatic; gene therapy; metastasis; ss.  
XX Homo sapiens.  
XX WO200151633-A2.

PD 19-JUL-2001.  
XX  
PF 16-JAN-2001; 2001WO-US001574.  
XX  
PR 14-JAN-2000; 2000US-00483672.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;  
PI Wang A, Meagher MJ;  
XX  
DR WPI; 2001-425873/45.  
XX  
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,  
PT monitoring and treating prostate cancer in a patient and for use in  
PT vaccines.  
XX  
PS Claim 1; Page 325; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode  
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
CC and can be used in vaccine production and gene therapy. (I), (II),  
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells  
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and  
CC the antibodies are also used in the detection of cancer in a patient. The  
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)  
CC and (II) can be used in vaccines. The antibodies or (I) can be used for  
CC monitoring the progression of cancer in a patient. (I) and (II) can also  
CC be used to improve diagnostic and therapeutic methods for prostate  
CC cancer. They can indicate the level of metastasis as well as the prostate  
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent  
CC polynucleotide and amino acid sequences used in the exemplification of  
CC the present invention  
XX

SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 4; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTTC 60  
Db 1 CAAATTTGAGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTTC 60  
Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAATTATATATCTA 120  
Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAATTATATATCTA 120  
Qy 121 CATTTACAGCATTTAAATATGTTTCAGCATGAAATATTAGTCACAGGGGAAGCTTAAATAA 180  
Db 121 CATTTACAGCATTTAAATATGTTTCAGCATGAAATATTAGTCACAGGGGAAGCTTAAATAA 180  
Qy 181 ATTAACAATGGAATAAAGATTGTCCTTAAATATAATCTACAAGAAGCTTTGATATTTG 240  
Db 181 ATTAACAATGGAATAAAGATTGTCCTTAAATATAATCTACAAGAAGCTTTGATATTTG 240  
Qy 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300  
Db 241 TTTTTCACAGTGAGCAATCTTATAAGTGTCTAAACCTTTTGGGGAAGCTATGGAA 300  
Qy 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Qy 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTGAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGTGTATCAAGTATAAA 480

QY 481 AGTTCTATAACTGTAGTNTACTTATTTTAATCCCAAGACAGT 526  
|||||  
Db 481 AGTTCTATAACTGTAGTNTACTTATTTTAATCCCAAGACAGT 526

## RESULT 3

AAS63752

ID AAS63752 standard; cDNA; 526 BP.

XX AAS63752;

XX AAS63752;

XX 29-JAN-2002 (first entry)

XX Human prostate cDNA sequence #304.

XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.

XX WO200173032-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009919.

XX 27-MAR-2000; 2000US-00536857.

XX 09-MAY-2000; 2000US-00568100.

XX 12-MAY-2000; 2000US-00570737.

XX 13-JUN-2000; 2000US-00593793.

XX 27-JUN-2000; 2000US-00605783.

XX 09-AUG-2000; 2000US-00636215.

XX 29-AUG-2000; 2000US-00651236.

XX 06-SEP-2000; 2000US-00657279.

XX 02-OCT-2000; 2000US-00679426.

XX 10-OCT-2000; 2000US-00685166.

XX 09-NOV-2000; 2000US-00709729.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

XX Fanger GR, Retter MW, Stolk JH, Day CH, Vedwick TS, Carter D;

XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2001-639232/73.

XX New human prostate-specific polypeptides and polynucleotides useful for

XX the diagnosis and treatment of cancer, especially prostate cancer.

XX Claim 1; Page 327; 579pp; English.

XX The invention relates to isolated prostate-specific polynucleotides,

XX polypeptides, fusion proteins of the polypeptides, antibodies raised

XX against the polypeptides (or antigenic epitopes derived from them) and

XX antigen-presenting cells expressing the polypeptides. The antibodies are

XX useful for detecting the presence of cancer, especially prostate cancer.

XX The polypeptides, polynucleotides and the antigen-presenting cells are

XX useful for stimulating and/or expanding T cells specific for a tumour

XX protein, and for inhibiting the development of cancer especially prostate

XX cancer. Compositions comprising the polynucleotide and/or polypeptide are

XX useful for stimulating an immune response, and for treating cancer. The

XX oligonucleotide is useful for detecting cancer. The present sequence is a

XX prostate specific polynucleotide of the invention

XX SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

XX Query Match 100.0%; Score 525; DB 4; Length 526;

XX Best Local Similarity 100.0%; Pred. No. 4.5e-115;

XX Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATTTCTGGGGCCATTTC 60

Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATTTCTGGGGCCATTTC 60

CC development of cancer in a patient. Antibodies specific for prostate  
CC specific proteins and oligonucleotides that hybridise to a polynucleotide  
CC that encodes a prostate specific protein are useful for detecting the  
CC presence or absence of a cancer or monitoring the progression the  
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,  
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the  
CC exemplification of the present invention

XX  
SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 4; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60  
Db 1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60  
QY 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120  
Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120  
QY 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180  
Db 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180  
QY 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGGAAGCTTTGATATTGT 240  
Db 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGGAAGCTTTGATATTGT 240  
QY 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300  
Db 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300  
QY 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480  
QY 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526  
Db 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526

RESULT 5  
AAH84973  
ID AAH84973 standard; cDNA; 526 BP.

XX  
AC AAH84973;

XX  
DT 25-SEP-2001 (first entry)

XX  
DE Human prostate-specific cDNA sequence P775P.

XX  
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;  
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;  
KW prostate specific antigen; PSA; ss.

XX  
OS Homo sapiens.

XX  
FN WO200134802-A2.

XX  
PD 17-MAY-2001.

XX  
PF 09-NOV-2000; 2000WO-US030904.

XX

PR 12-NOV-1999; 99US-00439313.  
PR 18-NOV-1999; 99US-00443686.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;  
XX  
XX WPI; 2001-308785/32.

XX  
PT Isolated polypeptide comprising at least an immunogenic portion of a  
PT prostate-specific protein, useful in the diagnosis and therapy of  
PT prostate cancer.

XX  
FS Claim 5; Page 224-225; 325pp; English.

XX  
CC The present invention describes an isolated polypeptide (P1) comprising  
CC at least an immunogenic portion of a prostate-specific protein, or its  
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and  
CC (N1) have cytostatic activity and can be used in vaccine production. The  
CC polypeptides, nucleic acids and antibodies from the present invention are  
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific  
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic  
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.  
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.  
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide  
CC and polypeptide sequences used in the exemplification of the present  
CC invention

XX  
SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 4; Length 526;

Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Db 1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

QY 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120

Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120

QY 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

Db 121 CATTTACAGCAATTTAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

QY 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGGAAGCTTTGATATTGT 240

Db 181 ATTAACATGGAATAAAGATTGTCTTAAATATAATCTACAAGGAAGCTTTGATATTGT 240

QY 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300

Db 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGCTATGGAA 300

QY 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Db 301 AAAATGGGGAAGCTCTGAAGGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480

Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTATAGTATCTGTGTATCAAGTATAA 480

QY 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526

Db 481 AGTTCTATAAAGCTAGTATCTTATTTTAAATCCCAAGCACAGT 526

RESULT 6

AAF86941  
ID AAF86941 standard; cDNA; 526 BP.  
XX  
AC AAF86941;  
XX  
DT 06-JUL-2001 (first entry)  
DE Human P775P inventive antigen coding sequence SEQ ID NO: 336.  
XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;  
KW chromosome 11p13; zinc finger transcription factor; ss.  
XX Homo sapiens.  
XX WO200125273-A2;  
XX 12-APR-2001.  
XX  
XX 04-OCT-2000; 2000WO-US027465.  
XX  
XX 04-OCT-1999; 99US-0157459P.  
XX (CORI-) CORIXA CORP.  
XX  
XX Skeiky YAW, Xu J, Cheever MA, Reed SG;  
XX WPI; 2001-328324/34.  
XX  
XX Polypeptide comprising part of the Wilms Tumor gene product sequence is  
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
PT and cancer associated with WT1.  
XX  
XX Disclosure; Page 214; 228pp; English.  
XX  
XX The present invention describes compositions comprising peptides derived  
CC from the Wilm's tumour protein WT1 and methods for their use in treating  
CC malignant diseases. Peptides derived from both the murine and human WT1  
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
CC and the protein was shown to be a zinc finger transcription factor. The  
CC immunogenic peptides of the invention are particularly useful in the  
CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
CC a coding sequence used in the exemplification of the invention  
XX  
SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;  
  
Query Match 100.0%; Score 525; DB 4; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CAAATTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTTATCTGGGGCCATTTC 60  
DB 1 CAAATTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTTATCTGGGGCCATTTC 60  
  
QY 61 TTTTGTAGCTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATCTA 120  
DB 61 TTTTGTAGCTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATATATATCTA 120  
  
QY 121 CATTTACAGATTTAAATAGTGTTCAGCATGAAATATATTAGCTACAGGGGAAGCTAAATAA 180  
DB 121 CATTTACAGATTTAAATAGTGTTCAGCATGAAATATATTAGCTACAGGGGAAGCTAAATAA 180  
  
QY 181 ATTAAACATGGAATAAAGATTTCTCTCTAAATATAATCTACAGAGAGCTTTTGATATTG 240  
DB 181 ATTAAACATGGAATAAAGATTTCTCTCTAAATATAATCTACAGAGAGCTTTTGATATTG 240  
  
QY 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAACCTATGGGAA 300  
DB 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAACCTATGGGAA 300  
  
QY 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
DB 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

361 TCTCTTTACAGGAGCTCTCTGAGCCCTTACAGAAATAGTGGCTGAGATTTCTGATTGC 420  
DB TCTCTTTACAGGAGCTCTCTGAGCCCTTACAGAAATAGTGGCTGAGATTTCTGATTGC 420  
  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTAGTATCTGTGTATCAAGTATAA 480  
DB 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTAGTATCTGTGTATCAAGTATAA 480  
  
QY 481 AGTTCTATAAATCTAGTNTACTTATTTTAAATCCCAAGCACAGT 526  
DB 481 AGTTCTATAAATCTAGTNTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 7  
ACA59560  
ID ACA59560 standard; cDNA; 526 BP.  
XX  
AC ACA59560;  
XX  
DT 10-JUN-2003 (first entry)  
DE Prostate cancer therapy associated cDNA #303.  
XX  
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;  
KW immunogen; cancer; prostate specific antigen; PSA;  
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;  
KW PSMA; gene; ss.  
XX Homo sapiens.  
XX  
XX US2002192763-A1.  
PN  
XX 19-DEC-2002.  
PD  
XX 29-JUN-2001; 2001US-00895793.  
PF  
XX 04-OCT-1999; 99US-0157455P.  
PR  
XX 04-OCT-2000; 2000US-00679272.  
PR  
XX 28-MAR-2001; 2001US-00822827.  
XX  
XX (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
XX  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;  
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TW;  
XX WPI; 2001-245062/25.  
DR  
XX Prostate specific protein and its encoding polynucleotide, useful for the  
PT treatment and diagnosis of prostate cancer.  
PT  
XX

PS Example 3; SEQ ID NO 311; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at [seqdata.uspto.gov/sequence.html?DocID=US20020192763](http://seqdata.uspto.gov/sequence.html?DocID=US20020192763)

XX Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 5; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60  
Db 1 CAAATTTGAGCCAAATGACATAGAAATTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATATATATATCTA 120  
Db 61 TTTTGACGTTTCTCTAAACTACTAAAGGCGATTAAATGATCCATAAATATATATATCTA 120

Qy 121 CATTTACAGCATTTAAATGTTTTCAGCATGAAATATTAGCTACAGGGGAGCTTAATAA 180  
Db 121 CATTTACAGCATTTAAATGTTTTCAGCATGAAATATTAGCTACAGGGGAGCTTAATAA 180

Qy 181 ATTAACATGGAAATGAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 240  
Db 181 ATTAACATGGAAATGAAGATTGTCTTAAATATAATCTACAAGAAGACTTTGATATTGG 240

Qy 241 TTTTTCACAAGTGAAGCACTTCTTAAAGTGTCATAACCTTTTGGGAAACTATGGAA 300  
Db 241 TTTTTCACAAGTGAAGCACTTCTTAAAGTGTCATAACCTTTTGGGAAACTATGGAA 300

Qy 301 AAAATGGGAAACTCTGAAGGTTTAAAGTATCTTACCTGAAAGCTACAGACTCCATAAC 360  
Db 301 AAAATGGGAAACTCTGAAGGTTTAAAGTATCTTACCTGAAAGCTACAGACTCCATAAC 360

Qy 361 TCTCTTTACAGGAGCTCTGAGGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTGAGGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTGTATGATCTGTGTATCAAGTATAAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTGTATGATCTGTGTATCAAGTATAAA 480

Qy 481 AGTTCTATAAAGCTAGTACTTATTTAAATCCCAAGACAGT 526  
Db 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGACAGT 526

XX US2002022248-A1.  
XX 21-FEB-2002.  
XX 12-JAN-2001; 2001US-00759143.  
XX 25-FEB-1997; 97US-00806099.  
XX 01-AUG-1997; 97US-00904804.  
XX 10-FEB-1998; 98US-00020956.  
XX 25-FEB-1998; 98US-00030607.  
XX 14-JUL-1998; 98US-00115453.  
XX 23-SEP-1998; 98US-00159812.  
XX 15-JAN-1999; 99US-00232149.  
XX 09-APR-1999; 99US-00288946.  
XX 13-JUL-1999; 99US-00352616.  
XX 12-NOV-1999; 99US-00439313.  
XX 18-NOV-1999; 99US-00443686.  
XX 14-JAN-2000; 2000US-00483672.  
XX 27-MAR-2000; 2000US-00536857.  
XX 09-MAY-2000; 2000US-00568100.  
XX 12-MAY-2000; 2000US-00570737.  
XX 13-JUN-2000; 2000US-00593793.  
XX 27-JUN-2000; 2000US-00605783.  
XX 10-AUG-2000; 2000US-00636215.  
XX 29-AUG-2000; 2000US-00651236.  
XX 06-SEP-2000; 2000US-00657279.  
XX 02-OCT-2000; 2000US-00679426.  
XX 10-OCT-2000; 2000US-00685166.  
XX XUJ/J/ XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD; Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D; Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA; WPI; 2002-255649/30.  
XX New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.  
XX Claim 1; SEQ ID NO 311; 87pp; English.  
XX The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention  
XX Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;  
SQ

Query Match 100.0%; Score 525; DB 6; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60  
|||



Db 1 CAAATTGACCAATGACATAGAAATTTTCAAAATCAAGAGCTTATTCTGGGCCATTTC 60  
Qy 61 TTTTGAGTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATTATCTA 120  
Db 61 TTTTGAGTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATTATCTA 120  
Qy 121 CAITTTACAGCAATTTAAATGTTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180  
Db 121 CAITTTACAGCAATTTAAATGTTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180  
Qy 181 ATTAAACATGGAATGAAGATTTGCTTAAATATATATCTACAGAGACCTTTGATTTTG 240  
Db 181 ATTAAACATGGAATGAAGATTTGCTTAAATATATATCTACAGAGACCTTTGATTTTG 240  
Qy 241 TTTTTCACAGTGAAGCATTTTATAAAGTGTCTAAACCTTTTGGGAAACTATCGGAA 300  
Db 241 TTTTTCACAGTGAAGCATTTTATAAAGTGTCTAAACCTTTTGGGAAACTATCGGAA 300  
Qy 301 AAAATGGGAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Qy 361 TCTCTTTACAGGAGCTCTGACGCCCTTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTGACGCCCTTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420  
Qy 421 ACAGCAAGAGCTTCTCATCTAARACCTTTCCCTTTTGTATCTGTATCAAGTATAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAARACCTTTCCCTTTTGTATCTGTATCAAGTATAA 480  
Qy 481 AGTTCTATAAAGTGTAGTNTACTTATTTAATCCCAAGCACAGT 526  
Db 481 AGTTCTATAAAGTGTAGTNTACTTATTTAATCCCAAGCACAGT 526

RESULT 9  
ACC95287  
ID ACC95287 standard; cDNA; 526 BP.  
AC ACC95287;  
XX  
XX  
28-AUG-2003 (first entry)  
XX Prostate tumour specific cDNA sequence SEQ ID 311.  
XX  
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;  
KW immune response; prostate cancer; ss.  
XX Homo sapiens.  
XX WQ200289747-A2.  
XX  
XX 14-NOV-2002.  
XX  
XX 09-MAY-2002; 2002WO-US014753.  
XX  
XX 09-MAY-2001; 2001US-00852911.  
XX  
XX 29-JUN-2001; 2001US-00895814.  
XX  
XX 10-DEC-2001; 2001US-00012896.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;  
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TW, Watanabe Y;  
PI Deng T;  
XX  
XX WPI; 2003-167130/16.  
XX  
XX New prostate-specific proteins and genes, useful in gene therapy,  
PT particularly for stimulating an immune response in a patient, or treating  
PT prostate cancer in a patient, as well as for diagnosing prostate cancer

PT in a patient.  
XX  
XX Example 3; Page 392-393; 691pp; English.  
XX  
CC The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to illustrate the invention  
XX  
SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;  
Query Match 100.0%; Score 525; DB 8; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAGCTTATTCTGGGCCATTTC 60  
Db 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAGCTTATTCTGGGCCATTTC 60  
Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATTATCTA 120  
Db 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATATATTATCTA 120  
Qy 121 CATTTACAGCATTTAAATGTTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180  
Db 121 CATTTACAGCATTTAAATGTTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAA 180  
Qy 181 ATTTAAACATGGAATGAAGATTTGCTTAAATATATATCTACAGAGACCTTTGATTTTG 240  
Db 181 ATTTAAACATGGAATGAAGATTTGCTTAAATATATATCTACAGAGACCTTTGATTTTG 240  
Qy 241 TTTTTCACAGTGAAGCATTTCTTAAAGTGTCTAATGATGTCATAACCTTTTGGGAACTATCGGAA 300  
Db 241 TTTTTCACAGTGAAGCATTTCTTAAAGTGTCTAATGATGTCATAACCTTTTGGGAACTATCGGAA 300  
Qy 301 AAAATGGGAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Qy 361 TCTCTTTACAGGAGCTCTGACGCCCTTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTGACGCCCTTACAGAAATGAGTGGCTGAGATTTCTGATTGC 420  
Qy 421 ACAGCAAGAGCTTCTCATCTAARACCTTTCCCTTTTGTATCTGTATCAAGTATAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAARACCTTTCCCTTTTGTATCTGTATCAAGTATAA 480  
Qy 481 AGTTCTATAAAGTGTAGTNTACTTATTTAATCCCAAGCACAGT 526  
Db 481 AGTTCTATAAAGTGTAGTNTACTTATTTAATCCCAAGCACAGT 526  
RESULT 10  
ADB13761  
ID ADB13761 standard; cDNA; 526 BP.  
XX  
AC ADB13761;  
XX  
XX 18-DEC-2003 (first entry)  
DT  
XX Human prostate specific cDNA P775P.  
XX  
XX Human; ss; prostate specific cDNA; cytostatic; immunostimulant;  
KW gene therapy; cell therapy; vaccine; T-cell epitope;  
KW class I major histocompatibility complex allele; MHC; prostate cancer;  
KW tumour; antigen presenting cell.  
XX  
XX Homo sapiens.  
XX  
XX US2003185830-A1.  
XX

PD 02-OCT-2003.

XX 12-NOV-2002; 2002US-00294025.

XX 25-FEB-1997; 97US-00806099.

PR 01-AUG-1997; 97US-00904804.

PR 09-FEB-1998; 98US-00020956.

PR 25-FEB-1998; 98US-00030607.

PR 14-JUL-1998; 98US-00115453.

PR 23-SEP-1998; 98US-00159812.

PR 15-JAN-1999; 99US-00232149.

PR 09-APR-1999; 99US-00288946.

PR 13-JUL-1999; 99US-00352616.

PR 12-NOV-1999; 99US-00439313.

PR 18-NOV-1999; 99US-00443686.

PR 14-JAN-2000; 2000US-00483672.

PR 27-MAR-2000; 2000US-00536857.

PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.

PR 13-JUN-2000; 2000US-00593793.

PR 27-JUN-2000; 2000US-00605783.

PR 09-AUG-2000; 2000US-00636215.

PR 29-AUG-2000; 2000US-00651236.

PR 06-SEP-2000; 2000US-00657279.

PR 02-OCT-2000; 2000US-00679426.

PR 10-OCT-2000; 2000US-00685166.

PR 09-NOV-2000; 2000US-00709729.

PR 12-JAN-2001; 2001US-00759143.

PR 09-FEB-2001; 2001US-00780669.

PR 09-MAY-2001; 2001US-00852911.

PR 29-JUN-2001; 2001US-00895814.

PR 10-DEC-2001; 2001US-00012896.

PR 09-MAY-2002; 2002US-00144678.

PA (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Kalos MD;

PI WPI; 2003-756193/71.

XX

PT New isolated polypeptide for use in a vaccine for stimulating an immune

PT response, or for treating or diagnosis cancer, preferably prostate

PT cancer.

XX

PS Example 3; Page; 101pp; English.

XX

CC The invention relates to an isolated polypeptide comprising no more than

CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The

CC peptides comprise a fragment ADB13563 of that contain naturally processed

CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)

CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific

CC cDNA, one of 648 disclosed as new. Also included are nucleic acids

CC encoding the proteins and peptides, expression vectors, a host cell

CC transformed with the vector, an isolated antibody (or antigen binding

CC fragment) that specifically binds to the protein or peptide, detecting

CC the presence of a cancer in a patient (comprising contacting a patient

CC sample with a binding agent that binds to the peptides or a polypeptide

CC appearing as ADB1358, detecting the amount of polypeptide that binds to

CC the agent and comparing the amount of polypeptide to a predetermined cut-

CC off value to determine the presence of cancer), a fusion protein

CC comprising the peptides or proteins, stimulating or expanding T cells

CC specific for a tumour protein comprising contacting T cells with the

CC peptides or the isolated T cell population, treating prostate cancer in a

CC patient comprising administering a composition comprising the peptides,

CC nucleic acids, antibodies or compounds, determining the presence of a

CC cancer in a patient and treating prostate cancer in a patient comprising

CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

CC from a patient with the peptides or antigen presenting cells that express

CC (the peptides so that the T cells proliferate, and administering the

CC proliferated T cells to the patient. The peptides (or an oligonucleotide

CC that hybridises to nucleic acid encoding them), is used to detect the

CC presence of cancer in a patient. The peptides, nucleic acids encoding, or

CC antigen-presenting cells expressing the nucleic acid, are used to

CC

CC stimulate or expand T cells specific for a tumour protein. The peptides,

CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen

CC presenting cells are used to stimulate an immune response or treat

CC prostate cancer in a patient. The present sequence is one of the

CC disclosed human prostate specific cDNAs. Note: Except where otherwise

CC indicated, the sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030195830.

XX

SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;

Query Match 100.0%; Score 525; DB 10; Length 526;

Best Local Similarity 100.0%; Pred. No. 4.5e-115;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAATGATCCATTAATATATATATCTA 120

Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAATGATCCATTAATATATATATCTA 120

Qy 121 CATTTACAGCATTTAAATATGTTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 180

Db 121 CATTTACAGCATTTAAATATGTTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 180

Qy 181 ATTAACATGGAATAAAGATTTTGTCTTAATATAATTAATCTACAAGAAGCTTTGATTTG 240

Db 181 ATTAACATGGAATAAAGATTTTGTCTTAATATAATTAATCTACAAGAAGCTTTGATTTG 240

Qy 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAACTATGGAA 300

Db 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAACTATGGAA 300

Qy 301 AAAATGGGAACTCTCGAAGGTTTAAAGTATCTTACTGAAGCTACAGACTCCATAACC 360

Db 301 AAAATGGGAACTCTCGAAGGTTTAAAGTATCTTACTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGGAGCTCTTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTTGATTGC 420

Db 361 TCTCTTTACAGGGAGCTCTTCGAGCCCTACAGAAATGAGTGGCTGAGATTCTTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTGTAGTATCTGTATCAAGTATAAA 480

Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTGTAGTATCTGTATCAAGTATAAA 480

Qy 481 AGTTCTATAAACTGTAGTACTTTTAAATCCCAAGACACAGT 526

Db 481 AGTTCTATAAACTGTAGTACTTTTAAATCCCAAGACACAGT 526

RESULT 11

ADG26177

ID ADG26177 standard; cDNA; 526 BP.

XX

AC ADG26177;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human prostate-specific cDNA #303.

XX

KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;

KW cytostatic.

XX

OS Homo sapiens.

XX

XX US2003157089-A1.

PD 21-AUG-2003.

XX

PF 09-MAY-2002; 2002US-00144678.

XX



PT partner, useful for diagnosing, preventing, or treating cancer, such as  
PT prostate cancer.  
XX  
XX Example 3; SEQ ID NO 311; 78pp; English.  
XX  
XX The present invention relates to prostate-specific fusion proteins and  
CC DNA encoding sequences. The fusion proteins can be used for diagnosing,  
CC preventing, or treating cancer, such as prostate cancer. The prostate-  
CC specific proteins were isolated from a human prostate tumor cDNA library.  
CC The present sequence is one such cDNA clone which was isolated in the  
CC prostate-specific cDNA library. Note: The sequence data for this patent  
CC did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
XX SQ Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;  
Query Match 100.0%; Score 525; DB 15; Length 526;  
Best Local Similarity 100.0%; Pred. No. 4.5e-115;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60  
Db 1 CAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60  
QY 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTA 120  
Db 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTA 120  
QY 121 CATTTACAGCATTTAAATGTTTCTCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 180  
Db 121 CATTTACAGCATTTAAATGTTTCTCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 180  
QY 181 ATTAACATGGAATGAAGATTGTCTTAAATATATATCTACAGAAGACTTTGATATTG 240  
Db 181 ATTAACATGGAATGAAGATTGTCTTAAATATATATCTACAGAAGACTTTGATATTG 240  
QY 241 TTTTTCAGAGTGAAGCATCTCTATAAGTGTCTATAAAGTGTCTATAAAGCTTTTGGGAA 300  
Db 241 TTTTTCAGAGTGAAGCATCTCTATAAAGTGTCTATAAAGCTTTTGGGAA 300  
QY 301 AAAATGGGAAACTCTGAAGGTTTAAAGTATCTTAACTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGAAACTCTGAAGGTTTAAAGTATCTTAACTGAAGCTACAGACTCCATAACC 360  
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTAACTCCCAAGACAGT 526  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTAACTCCCAAGACAGT 526  
QY 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAACTCCCAAGACAGT 526  
Db 481 AGTTCTATAAAGTGTAGTNTACTTATTTTAACTCCCAAGACAGT 526  
RESULT 13  
ID ABV27596 standard; cDNA; 1203 BP.  
XX  
XX AC ABV27596;  
XX  
XX 16-SEP-2002 (first entry)  
XX  
XX Human prostate expression marker cDNA 27587.  
XX  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200160860-A2.

XX 23-AUG-2001.  
XX  
XX 20-FEB-2001; 2001WO-US005171.  
XX  
XX 17-FEB-2000; 2000US-0183319P.  
XX 16-MAR-2000; 2000US-0189862P.  
XX 25-MAY-2000; 2000US-0207454P.  
XX 09-JUN-2000; 2000US-0211314P.  
XX 18-JUL-2000; 2000US-0219007P.  
XX 13-DEC-2000; 2000US-0255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
XX Claim 1; Page 5644; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
XX SQ Sequence 1203 BP; 395 A; 209 C; 199 G; 391 T; 0 U; 9 Other;  
Query Match 90.9%; Score 477.2; DB 5; Length 1203;  
Best Local Similarity 98.8%; Pred. No. 1.2e-103;  
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;  
QY 1 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60  
Db 342 CAAATTTGAGCCAAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 401  
QY 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTA 120  
Db 402 TTTTGACGTTTCTCTAACTACTAAAGAGGCAATTAATGATCCATAAATTTATATCTA 461  
QY 121 CATTTACAGCATTTAAATGTTTCTCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 180  
Db 462 CATTTACAGCATTTAAATGTTTCTCAGCATGAAATATTAGCTACAGGGAAGCTTAAATAA 521  
QY 181 ATTAACATGGAATGAAGATTGTCTTAAATATATATCTACAGAAGACTTTGATATTG 240  
Db 522 ATTAACATGGAATGAAGATTGTCTTAAATATATATCTACAGAAGACTTTGATATTG 581  
QY 241 TTTTTCAGAGTGAAGCATCTCTATAAAGTGTCTATAAAGCTTTTGGGAAACTATGGAA 300  
Db 582 TTTTTCAGAGTGAAGCATCTCTATAAAGTGTCTATAAAGCTTTTGGGAAACTATGGAA 641  
QY 301 AAAATGGGAAACTCTGAAGGTTTAAAGTATCTTAACTGAAGCTACAGACTCCATAACC 360  
Db 642 AAAATGGGAAACTCTGAAGGTTTAAAGTATCTTAACTGAAGCTACAGACTCCATAACC 701  
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420  
Db 702 TCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 761  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTCCCTTTTAACTCCCAAGATATAA 480

Db 762 ATAGC-AGAGCTTCTCATCTAAACCCTTTCCCTTTTAGTGTCTGTATC-AGTATAAA 819  
QY 481 AGTTCTATAAAGTGTAGTACTTATTTAAATCCCAA 518  
Db 820 AGTTCTATAAAGTGTAGT-TACTTATTTAAATCCCAA 856

RESULT 14  
ABV28357  
ID ABV28357 standard; cDNA; 1203 BP.  
XX AC ABV28357;  
XX DT 16-SEP-2002 (first entry)  
XX DE Human prostate expression marker cDNA 28348.  
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynanamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200160860-A2.  
XX PD 23-AUG-2001.  
XX PF 20-FEB-2001; 2001WO-US005171.  
XX PR 17-FEB-2000; 2000US-0183319P.  
PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX Claim 1; Page 5909; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (i) is also useful as a pharmacodynanamic or pharmacogenomic marker  
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Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;  
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QY 481 AGTTCTATAAAGTGTAGTACTTATTTAAATCCCAA 518  
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XX AC ABV22542;  
XX DT 13-SEP-2002 (first entry)  
XX DE Human prostate expression marker cDNA 22533.  
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynanamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200160860-A2.  
XX PD 23-AUG-2001.  
XX PF 20-FEB-2001; 2001WO-US005171.  
XX PR 17-FEB-2000; 2000US-0183319P.  
PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX Claim 1; Page 3939; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
SQ Sequence 1203 BP; 395 A; 209 C; 199 G; 391 T; 0 U; 9 Other;

Query Match 90.9%; Score 477.2; DB 5; Length 1203;  
Best Local Similarity 98.8%; Pred. No. 1.2e-103;  
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QY 1 CAATTTTCAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60  
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342 CAATTTGAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 401  
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GenCore version 5.1.9  
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Scoring table: IDENTITY NUC  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 13: gb\_in.\*  
 14: gb\_om.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	525	100.0	526	2	AR237399 Sequence
3	525	100.0	526	2	AR278423 Sequence
4	525	100.0	526	2	AR367119 Sequence
5	525	100.0	526	2	AR371015 Sequence
6	525	100.0	526	2	AR400155 Sequence
7	525	100.0	526	2	AR405422 Sequence
8	525	100.0	526	2	AR439626 Sequence
9	525	100.0	526	2	AR563802 Sequence
10	525	100.0	526	2	AR588788 Sequence
11	525	100.0	526	2	AR605608 Sequence
12	525	100.0	526	2	AR656947 Sequence
13	525	100.0	526	2	AR716854 Sequence
14	525	100.0	526	2	AX106198 Sequence
15	525	100.0	526	2	AX106530 Sequence
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17	525	100.0	526	2	AX200681 Sequence
18	525	100.0	526	2	AX267337 Sequence

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21	478.8	91.2	182817	12	AC080181
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23	477.2	90.9	1203	2	CO490668
24	477.2	90.9	1203	2	CO495743
25	477.2	90.9	1203	2	CO496503
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27	474	90.3	176156	5	CNS08CCG
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## ALIGNMENTS

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 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

BD242216 526 bp DNA linear PAT 17-JUL-2003  
 Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.

BD242216.1 GI:33051986  
 JP 2002520054-A/303.  
 Homo sapiens (human)

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 526)  
 Dillon,D.C., Harlocker,S.L., Yuqiu,J., Xu,J. and Mitcham,J.L.  
 Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use  
 Patent: JP 2002520054-A 303 09-JUL-2002;  
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 OS Homo sapiens (human)  
 PN JP 2002520054-A/303  
 PD 09-JUL-2002  
 PF 14-JUL-1999 JP 2000560247  
 PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR  
 23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR  
 15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR  
 09-APR-1999 US 09/288946  
 PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI  
 JIANGCHUN XU,  
 JENNIFER LYNN MITCHAM  
 PI C12N15/09,A61K39/00,A61K39/395,C07K14/47,C07K16/30,  
 C12N5/10,  
 PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,  
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 PC C12N5/00  
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Query Match      100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
LOCUS AR278423 526 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 311 from patent US 6512094.
ACCESSION AR278423
VERSION AR278423.1 GI:29712669
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T. and Henderson, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 311 28-JAN-2003;
Corixa Corporation; Seattle, WA
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Query Match      100.0%; Score 525; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 2.3e-138;
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Db 481 AGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAGACAGT 526

RESULT 2
AR237399
LOCUS AR237399 526 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 311 from patent US 6465611.
ACCESSION AR237399
VERSION AR237399.1 GI:27282057
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D. C. and Mitcham, J. L.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6465611-A 311 15-OCT-2002;
Corixa Corporation; Seattle, WA
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DEFINITION Sequence 311 from patent US 6329505.  
ACCESSION AR367119  
VERSION AR367119.1 GI:34600094  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yuqiu, J.,  
Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stoik, J.A. and  
Day, C.H.  
TITLE Compositions and methods for therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: US 6329505-A 311 11-DEC-2001;  
Corixa Corporation; Seattle, WA  
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ORIGIN  
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ACCESSION AR371015  
VERSION AR371015.1 GI:34607908  
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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L. and Yuqiu, J.  
TITLE Prostate specific fusion protein compositions  
JOURNAL Patent: US 6395278-A 311 28-MAY-2002;  
Corixa Corporation; Seattle, WA  
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QY 481 AGTTCTATAAATCTAGTNTACTTATTTAATCCCAAGACACAGT 526
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LOCUS AR400155 526 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 311 from patent US 6620922.
ACCESSION AR400155
VERSION AR400155.1 GI:40143264
KEYWORDS
SOURCE
ORGANISM
Unclausified.
REFERENCE
1 (bases 1 to 526)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 311 16-SEP-2003;
Corixa Corporation; Seattle, WA
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 311 from patent US 6630305.
ACCESSION AR405422
VERSION AR405422.1 GI:40154259
KEYWORDS
SOURCE
ORGANISM
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Unclausified.
REFERENCE
1 (bases 1 to 526)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 311 07-OCT-2003;
Corixa Corporation; Seattle, WA;
WOX;
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 311 from patent US 6664377.
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ACCESSION AR439626  
VERSION AR439626.1 GI:42665535  
KEYWORDS  
SOURCE Unknown:  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Xu, J.  
TITLE Compounds for immunotherapy of prostate cancer and methods for their use  
JOURNAL Patent: US 6643777-A 311 16-DEC-2003;  
Corixa Corporation; Seattle, WA;  
WOX;  
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DEFINITION Sequence 311 from patent US 6759515.  
ACCESSION AR563802  
VERSION AR563802.1 GI:53978853  
KEYWORDS  
SOURCE Unknown:  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,  
Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6800746-A 311 05-OCT-2004;  
Corixa Corporation; Seattle, WA  
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;  
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DEFINITION Sequence 311 from patent US 6800746.  
ACCESSION AR588788  
VERSION AR588788.1 GI:56635685  
KEYWORDS  
SOURCE Unknown:  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,  
Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6800746-A 311 05-OCT-2004;  
Corixa Corporation; Seattle, WA  
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Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,  
Hepler, W.T. and Henderson, R.A.  
Compositions and methods for the therapy and diagnosis of prostate cancer  
Patent: US 6759515-A 311 06-JUL-2004;  
Corixa Corporation; Seattle, WA  
Location/Qualifiers  
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LOCUS AR588788  
DEFINITION Sequence 311 from patent US 6800746.  
ACCESSION AR588788  
VERSION AR588788.1 GI:56635685  
KEYWORDS  
SOURCE Unknown:  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,  
Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6800746-A 311 05-OCT-2004;  
Corixa Corporation; Seattle, WA  
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VERSION AR716854.1 GI:77365503
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 526)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T., Henderson, R.A., Hural, J., McNeill, P.D., Houghton, R.L.,
Vinals, Y. de Bassols, C., Foy, T.M., Watanabe, Y. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6943236-A 311 13-SEP-2005;
Corixa Corporation; Seattle, WA
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RESULT 14
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ACCESSION AX106198
VERSION AX106198.1 GI:13921888
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Skeiky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.
TITLE Compositions and methods for wt1 specific immunotherapy
JOURNAL Patent: WO 0125273-A 336 12-APR-2001;
CORIXA CORPORATION (US)
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GenCore version 5.1.9  
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Perfect score: 525  
Sequence: 1 caaatgtgccaatgacat.....tttaatccccaagcacagt 526

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3050214 seqs, 1077301958 residues

Total number of hits satisfying chosen parameters: 6100428

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	100.0	526	7	US-11-344-932-311
2	469.2	89.4	3434	7	US-11-344-932-476
3	261.6	49.8	2414	7	US-11-344-932-475
4	109	20.8	1594	7	US-11-344-932-474
5	45.8	8.7	4022	6	US-10-517-441-458
6	45.8	8.7	4022	6	US-10-517-441-732
7	42.8	8.2	13286	6	US-10-517-441-746
8	42.4	8.1	2000	10	US-11-299-286-2856
9	42.4	8.1	6432	6	US-10-517-441-606
10	42.4	8.1	6432	6	US-10-506-111-346
11	42.2	8.0	16579	6	US-10-517-441-290
12	42.2	8.0	16579	6	US-10-517-441-564
13	42.2	8.0	16579	6	US-10-506-089-9
14	42.2	8.0	16579	6	US-10-506-089-19
15	42.2	8.0	16579	6	US-10-506-111-174
16	42.2	8.0	16579	6	US-10-506-111-302
17	42	8.0	189056	8	US-11-266-748A-29044
18	42	8.0	1317241	10	US-11-184-236-73
19	41.4	7.9	107543	6	US-10-539-228-706
20	41.2	7.8	13286	6	US-10-517-441-472
21	41.2	7.8	97415	6	US-10-539-228-287
22	41	7.8	8085	6	US-10-506-111-207

Sequence 335, App  
Sequence 380, App  
Sequence 3267, App  
Sequence 1598, App  
Sequence 4586, App  
Sequence 4, Appl  
Sequence 471243, App  
Sequence 12707, A  
Sequence 294, App  
Sequence 568, App  
Sequence 1267, App  
Sequence 6524, App  
Sequence 201282, App  
Sequence 201283, App  
Sequence 314, App  
Sequence 1313, App  
Sequence 7775, App  
Sequence 332, App  
Sequence 218, App  
Sequence 1211, App  
Sequence 6304, App  
Sequence 5907, App

## ALIGNMENTS

RESULT 1  
US-11-344-932-311  
; Sequence 311, Application US/11344932  
; Publication No. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Deng, Fa  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C32  
; CURRENT FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: 10/144,932  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 10/012,896  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 09/895,814  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/852,911  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: 09/780,669  
; PRIOR FILING DATE: 2001-02-09



```

; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 499
; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-311

Query Match      100.0%; Score 525; DB 7; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.1e-122; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTTCTCTAACTACTAAAGAGGCAATTAATGCCATAAATATATATATCTA 120
Db 61 TTTTGACGTTTTCTCTAACTACTAAAGAGGCAATTAATGCCATAAATATATATATCTA 120

Qy 121 CATTTACAGCAATTTAAATGTCTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTACAGCAATTTAAATGTCTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

Qy 181 ATTTAAACATGGAATTAAGATTTGTCTTAAATATAATCTACAAGAGACTTTTGATATTG 240
Db 181 ATTTAAACATGGAATTAAGATTTGTCTTAAATATAATCTACAAGAGACTTTTGATATTG 240

Qy 241 TTTTTCACAGTGAAGCAATCTTTATAAGTGTCATAAACCCTTTTGGGGAACCTATGGAA 300
Db 241 TTTTTCACAGTGAAGCAATCTTTATAAGTGTCATAAACCCTTTTGGGGAACCTATGGAA 300

Qy 301 AAAATGGGGAAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGAGCTCCTCAGGCCCTTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCCTCAGGCCCTTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480
Db 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480

Qy 481 AGTTCTATAAATGTAGTNTACTTATTTTAAATCCCCCAAGCACAGT 526
Db 481 AGTTCTATAAATGTAGTNTACTTATTTTAAATCCCCCAAGCACAGT 526
```

RESULT 2  
US-11-344-932-476/C  
; Sequence 476, Application US/11344932  
; Publication No. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.

```

; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Wang, AiJun
; APPLICANT: Wang, Li, Samuel X.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Deng, Ia
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 476
; LENGTH: 3434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-344-932-476

Query Match      89.4%; Score 469.2; DB 7; Length 3434;
Best Local Similarity 97.9%; Pred. No. 7.4e-108; Indels 3; Gaps 3;
Matches 507; Conservative 0; Mismatches 8;

Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 3062 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 3003

Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATATCTA 120
Db 3002 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 2943

Qy 121 CATTTACAGCAATTTAAATGTCTCAGCATCAAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 2942 CATTTACAGCAATTTAAATGTCTCAGCATCAAAATATTAGCTACAGGGGAAGCTAAATAA 2883

Qy 181 ATTTAAACATGGAATTAAGACTTTGTCTTTAAATATAATCTACAAGAGACTTTTGATATTG 240
Db 181 ATTTAAACATGGAATTAAGACTTTGTCTTTAAATATAATCTACAAGAGACTTTTGATATTG 240
```



Db 2882 ATTAACATGGAATAAGATTTGCTCTTAAAAATAATCTACAGAAGACTTTTGATATTG 2823  
Qy 241 TTTTTCACAGTGAAGCATTTCTATATAAGTGTCATTAACCTTTTGGGGAACCTATCGGAA 300  
Db 2822 TTTTTCACAGTGAAGCATTTCTATATAAGTGTCATTAACCTTTTGGGGAACCTATCGGAA 2763  
Qy 301 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTAACTGAAGCTACAGACTCCATAACC 360  
Db 2762 AAAATGGGAACTCTGAAGGGTTTAAAGTATCTTAACTGAAGCTACAGACTCCATAACC 2703  
Qy 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGATGGCTGAGATCTTGATTGC 420  
Db 2702 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGATGGCTGAGATCTTGATTGC 2643  
Qy 421 ACAGCAAGAGCTCTCATCTAAACCTTTCCCTTTTAACTGATCTGATCAAGTATAAA 480  
Db 2642 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTAACTGATCTGATCAAGTATAAA 2585  
Qy 481 AGTCTATAAATCTGATGTTACTTATTTTAAATCCCAA 518  
Db 2584 AGTCTATAAATCTGATGTTACTTATTTTAAATCCCAA 2548

## RESULT 3

US-11-344-932-475/c  
; Sequence 475, Application US/11344932  
; Publication No. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Deng, Ta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C32  
; CURRENT APPLICATION NUMBER: US/11/344,932  
; CURRENT FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: 10/144,678  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 10/012,896  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 09/895,814  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/852,911  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: 09/780,669  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/759,143  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/709,729  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 09/685,166

; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 09/679,426  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/657,279  
; PRIOR FILING DATE: 2000-09-06  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1033  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 475  
; LENGTH: 2414  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 33  
; OTHER INFORMATION: n = A,T,C or G  
US-11-344-932-475  
Query Match 49.8%; Score 261.6; DB 7; Length 2414;  
Best Local Similarity 98.1%; Pred. No. 7.3e-56;  
Matches 264; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATCTGGGGCCATTTC 60  
Db 282 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATCTGGGGCCATTTC 223  
Qy 61 TTTTGACGTTTTCTCTAACTACTAAAGAGGCATTAATGATCCATAAAATTTATATTATCTA 120  
Db 222 TTTTGACGTTTTCTCTAACTACTAAAGAGGCATTAATGATCCATAAAATTTATATTATCTA 163  
Qy 121 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 180  
Db 162 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 103  
Qy 181 ATTAACATGGAATAAGATTTGTCCTTTAAATATATCTACAGAGACTTTTGATATTG 240  
Db 102 ATTAACATGGAATAAGATTTGTCCTTTAAATAATCTACAGAGACTTTTGATATTG 43  
Qy 241 TTTTTCACAAGTGAAGCATTTCTTATAAAG 269  
Db 42 TTTTTCACANGTGAAGCATTTCTTATAAAG 14

## RESULT 4

US-11-344-932-474/c  
; Sequence 474, Application US/11344932  
; Publication No. US20060269532A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Deng, Ta

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C32
; CURRENT APPLICATION NUMBER: US/11/344,932
; PRIOR FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: 10/144,678
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/012,896
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 09/895,814
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/852,911
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/780,669
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/759,143
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/709,729
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/685,166
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 09/679,426
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/657,279
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-344-932-474

Query Match      20.8%; Score 109; DB 7; Length 1594;
Best Local Similarity 100.0%; Pred. No. 1.2e-17; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 109 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 50

Qy 61 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAAT 109
Db 49 TTTTGACGTTTCTCTAACTACTAAAGAGGCATTAAATGATCCATAAAT 1

RESULT 5
; Sequence 458, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 732
; LENGTH: 4022
```

```
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 458
; LENGTH: 4022
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1299, 1372, 1784, 3008, 3018)
; OTHER INFORMATION: unknown base
US-10-517-441-458

Query Match      8.7%; Score 45.8; DB 6; Length 4022;
Best Local Similarity 51.2%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 102;

Qy 69 TTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATTTATATTCTTACATTTACA 128
Db 2161 TTTAAATTTTAAATAAATAATACATAAAAAATAAATACTATTACATACGAAAAATACATTAATT 2102

Qy 129 GCATTTAAATGTTCTCAGCATGAAATATTAGCTACAGGGGAAGCTTTTGATATTTGTTTTTTCAC 188
Db 2101 TAATTTAATCTTTAAATAAAAAAACTATTAAAAATTTATCTTTAAATTTAAATTTAATTAT 2042

Qy 189 TGGGAATAAGATTTGCTCTTAAATAATAATATCTACAGAAGAGCTTTTGATATTTGTTTTTTCAC 248
Db 2041 TAAATTAATAAATTAATAAATCTTATAAATAATAATAATAAATAAATAAATAAATAAATAAATT 1982

Qy 249 AAGTGAAGCATTCTTATAAAGTGTCTATAA 277
Db 1981 AAATCAATTTTAAATTAATAAATTTATCATAA 1953

RESULT 6
; Sequence 732, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 732
; LENGTH: 4022
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; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MAX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 606
; LENGTH: 6432
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-606

Query Match      8.1%; Score 42.4; DB 6; Length 6432;
Best Local Similarity 47.6%; Pred. No. 0.9;
Matches 159; Conservative 0; Mismatches 171; Indels 4; Gaps 1;

Qy 37 AGAGCTTATCTGGGGCCATTTCTTTGACGTTTCTTAACTAACTAAAGAGGCATTA 96
Db 3583 ACAATTTTCTCTAAATCTTTTATACCTAAATTCATTCATCCACAAATATTTTATTA 3524

Qy 97 ATGATCCATAAATTATATATATATATATATATATATATATATATATATATATATAT 156
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Qy 157 TTAGCTACAGGGGAAGCTAAATATAATATAATATAATATAATATAATATAATATAAT 216
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Qy 217 TCTCAAGAAGACTTTTGATATTTGTTTTCACAGTGAAGCATTTCTTATAAGTGTCTA 276
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Qy 277 ACCTTTTGGGGAACCTATGGGAAAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTA 336
Db 3343 ----TAATACAAAATCTACTCATATAAATAAATAAATAAATAAATAAATAAATAA 3288

Qy 337 CTGAAGCTACAGACTCCATAACCTCTCTTTTACA 370
Db 3287 ATTCATCCACAAAACCAAAATTAACATAATA 3254

RESULT 10
US-10-506-111-346/c
; Sequence 346, Application US/10506111
; Publication No. US20060246433A1
; GENERAL INFORMATION:
; APPLICANT: Adorian, Peter
; APPLICANT: Burger, Matthias
; APPLICANT: Maier, Sabine

```

```

; APPLICANT: Nimmrich, Inko
; APPLICANT: Becker, Evelyne
; APPLICANT: Lesche, Ralf
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Armin
; TITLE OF INVENTION: METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF A COLON CELL PROLIFE
; TITLE OF INVENTION: DISORDER
; FILE REFERENCE: 47675-84/P094US
; CURRENT APPLICATION NUMBER: US/10/506,111
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PCT/EP03/02035
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: EP02004551.4
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 1030
; SEQ ID NO 346
; LENGTH: 6432
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-506-111-346

Query Match      8.1%; Score 42.4; DB 6; Length 6432;
Best Local Similarity 47.6%; Pred. No. 0.9;
Matches 159; Conservative 0; Mismatches 171; Indels 4; Gaps 1;

Qy 37 AGAGCTTATCTGGGGCCATTTCTTTGACGTTTCTTAACTAACTAAAGAGGCATTA 96
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Qy 97 ATGATCCATAAATTATATATATATATATATATATATATATATATATATATATATAT 156
Db 3523 AACATCAATTATATATATATATATATATATATATATATATATATATATATATATAT 3464

Qy 157 TTAGCTACAGGGGAAGCTAAATATAATATAATATAATATAATATAATATAATATAAT 216
Db 3463 ATACTACCTCCAAATAATTTAAATTAATATAATATAATATAATATAATATAATATA 3404

Qy 217 TCTCAAGAAGACTTTTGATATTTGTTTTCACAGTGAAGCATTTCTTATAAGTGTCTA 276
Db 3403 CACAAATAATATATAAATTTACAACTATATAAATAAATAAATAAATAAATAAATAA 3344

Qy 277 ACCTTTTGGGGAACCTATGGGAAAAATGGGAAACTCTGAAGGGTTTAAAGTATCTTA 336
Db 3343 ----TAATACAAAATCTACTCATATAAATAAATAAATAAATAAATAAATAAATAA 3288

Qy 337 CTGAAGCTACAGACTCCATAACCTCTCTTTTACA 370
Db 3287 ATTCATCCACAAAACCAAAATTAACATAATA 3254

RESULT 11
US-10-517-441-290
; Sequence 290, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MAX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: December 31, 2006, 12:22:01 ; Search time 837.563 Seconds  
(without alignments)  
7716.790 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
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11: /EMC\_Celerra\_SID83/ptodata/2/pubpna/US10F\_PUBCOMB.seq:  
12: /EMC\_Celerra\_SID83/ptodata/2/pubpna/US10G\_PUBCOMB.seq:  
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14: /EMC\_Celerra\_SID83/ptodata/2/pubpna/US11B\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	100.0	526	3	US-09-759-143-311
2	525	100.0	526	3	US-09-780-669-311
3	525	100.0	526	3	US-09-822-827-311
4	525	100.0	526	3	US-09-232-880-311
5	525	100.0	526	3	US-09-895-793-311
6	525	100.0	526	3	US-09-895-814-311
7	525	100.0	526	6	US-10-012-896-311
8	525	100.0	526	6	US-10-010-940-311
9	525	100.0	526	7	US-10-144-678A-311
10	525	100.0	526	7	US-10-294-025-311
11	525	100.0	526	16	US-11-234-786-311
12	477.2	90.9	1203	9	US-10-357-930-21765
13	477.2	90.9	1203	9	US-10-357-930-22535
14	477.2	90.9	1203	9	US-10-357-930-27610
15	477.2	90.9	1203	9	US-10-357-930-28370
16	469.2	89.4	634	9	US-10-357-930-43052
17	469.2	89.4	3434	3	US-09-759-143-476

ALIGNMENTS

RESULT 1  
US-09-759-143-311

Sequence 311, Application US/09759143  
Patent No. US2002022248A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C23  
CURRENT APPLICATION NUMBER: US/09/759,143  
CURRENT FILING DATE: 2001-01-12  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 311  
LENGTH: 526  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)...(526)  
OTHER INFORMATION: n = A,T,C or G  
US-09-759-143-311  
Query Match 100.0%; Score 525; DB 3; Length 526;

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Sequence 13042, A  
Sequence 34190, A  
Sequence 3873, App  
Sequence 438, App  
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Sequence 475, App  
Sequence 2, Appli  
Sequence 2, Appli  
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Sequence 474, App

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Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTTC 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 CAAATTTGAGGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTTC 60
Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGATTAATGATCCATAAATATATATATCTA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 TTTTGACGTTTCTCTAAACTACTAAAGAGGATTAATGATCCATAAATATATATATCTA 120
Qy 121 CATTTACAGCATTTAAATATGTTTCAGCATCAAAATATAGCTACAGGGGAAGCTTAAATAA 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 CATTTACAGCATTTAAATATGTTTCAGCATCAAAATATAGCTACAGGGGAAGCTTAAATAA 180
Qy 181 ATTAACATGGAATAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTTG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 ATTAACATGGAATAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTTG 240
Qy 241 TTTTTCACAGTGGAAGCATTTCTTATAAAGTGTCATAACCTTTTGGGGAAACTATGGGAA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 TTTTTCACAGTGGAAGCATTTCTTATAAAGTGTCATAACCTTTTGGGGAAACTATGGGAA 300
Qy 301 AAAATGGGGAACCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 AAAATGGGGAACCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGCTCCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
421 TCTCTTTACAGGAGCTCCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTAAAGTATCTGATCAAGTATATAA 480
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481 AGTTCTATAAAGCTGAGTNTACTTTTAAATCCCAAGCACAGT 526
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## RESULT 2

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US-09-780-669-311
; Sequence 311, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
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LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-780-669-311

Query Match 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTTC 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 CAAATTTGAGGCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTTC 60
Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGATTAATGATCCATAAATATATATATCTA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 TTTTGACGTTTCTCTAAACTACTAAAGAGGATTAATGATCCATAAATATATATATCTA 120
Qy 121 CATTTACAGCATTTAAATATGTTTCAGCATCAAAATATAGCTACAGGGGAAGCTTAAATAA 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 CATTTACAGCATTTAAATATGTTTCAGCATCAAAATATAGCTACAGGGGAAGCTTAAATAA 180
Qy 181 ATTAACATGGAATAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTTG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 ATTAACATGGAATAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTTGATATTTG 240
Qy 241 TTTTTCACAGTGGAAGCATTTCTTATAAAGTGTCATAACCTTTTGGGGAAACTATGGGAA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 TTTTTCACAGTGGAAGCATTTCTTATAAAGTGTCATAACCTTTTGGGGAAACTATGGGAA 300
Qy 301 AAAATGGGGAACCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 AAAATGGGGAACCTCTGAAGGTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Qy 361 TCTCTTTACAGGAGCTCCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 TCTCTTTACAGGAGCTCCTGAGGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTAAAGTATCTGATCAAGTATATAA 480
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## RESULT 3

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US-09-822-827-311
; Sequence 311, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-827-311
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; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
Db 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120

Qy 121 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180

Qy 181 ATTAACATGGAATAAAGATTGTCCTTTAAATATAATCTACAAGAAGACTTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGTCCTTTAAATATAATCTACAAGAAGACTTTTGATATTG 240

Qy 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGACTATGGAA 300
Db 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGACTATGGAA 300

Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
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Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTTAACTCCCAAGACACAGT 526
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; Sequence 311, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895.814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-814-311

Query Match      100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60
Db 1 CAAATTTGAGCCAAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60

Qy 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120
Db 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120

Qy 121 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 121 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAATATTAGCTACAGGGGAAGCTAAATAA 180

Qy 181 ATTAACATGGAATAAAGATTGTCCTTTAAATATAATCTACAAGAAGACTTTTGATATTG 240
Db 181 ATTAACATGGAATAAAGATTGTCCTTTAAATATAATCTACAAGAAGACTTTTGATATTG 240

Qy 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGACTATGGAA 300
Db 241 TTTTTCACAGTGAAGCAATCTTATAAAGTGTCAATACCTTTTGGGGAAGACTATGGAA 300

Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGAGCTCCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
Db 361 TCTCTTTACAGGAGCTCCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTTAACTCCCAAGACACAGT 526
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTTAACTCCCAAGACACAGT 526

Qy 481 AGTTCTATAAACTGTAGTNTACTTATTTTAACTCCCAAGACACAGT 526
Db 481 AGTTCTATAAACTGTAGTNTACTTATTTTAACTCCCAAGACACAGT 526

RESULT 7
US-10-012-896-311
; Sequence 311, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
```

APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Foy, Teresa  
APPLICANT: Fanger, Gary R.  
APPLICANT: Wantanabe, Yoshihiro  
APPLICANT: Meagher, Madeleine Joy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C27  
CURRENT APPLICATION NUMBER: US/10/012,896  
CURRENT FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 1011  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 311  
LENGTH: 526  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 499  
OTHER INFORMATION: n = A,T,C or G  
US-10-012-896-311

Query Match 100.0%; Score 525; DB 6; Length 526;  
Best Local Similarity 100.0%; Pred. No. 6.7e-113;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60  
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60  
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120  
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120  
QY 121 CATTTACAGCATTTAAATATGTTTCAGCATGAATATTTAGCTACAGGGAAGCTAAATAA 180  
Db 121 CATTTACAGCATTTAAATATGTTTCAGCATGAATATTTAGCTACAGGGAAGCTAAATAA 180  
QY 181 ATTAAACATGGAATAAAGATTTGTCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240  
Db 181 ATTAAACATGGAATAAAGATTTGTCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240  
QY 241 TTTTTCACAAGTGAAGCATTTCTATAAAGTGTCAATACCTTTTGGGGAAACTATGGGAA 300  
Db 241 TTTTTCACAAGTGAAGCATTTCTATAAAGTGTCAATACCTTTTGGGGAAACTATGGGAA 300  
QY 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTCACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTCACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480  
QY 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526  
Db 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526

RESULT 8

US-10-010-940-311  
Sequence 311, Application US/10010940  
Publication No. US20030088062A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang Yuqui  
APPLICANT: Reed, Steven G.  
APPLICANT: Kalos, Michael  
APPLICANT: Fanger, Gary  
APPLICANT: Retter, Mark  
APPLICANT: Solk, John  
APPLICANT: Day, Craig  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427D3  
CURRENT APPLICATION NUMBER: US/10/010,940  
CURRENT FILING DATE: 2001-12-05  
NUMBER OF SEQ ID NOS: 575  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 311  
LENGTH: 526  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(526)  
OTHER INFORMATION: n = A,T,C or G  
US-10-010-940-311

Query Match 100.0%; Score 525; DB 6; Length 526;  
Best Local Similarity 100.0%; Pred. No. 6.7e-113;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60  
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCCATTTTC 60  
QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120  
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGCCATTAATGATCCATAAATATATATCTA 120  
QY 121 CATTTACAGCATTTAAATATGTTTCAGCATGAATATTTAGCTACAGGGAAGCTAAATAA 180  
Db 121 CATTTACAGCATTTAAATATGTTTCAGCATGAATATTTAGCTACAGGGAAGCTAAATAA 180  
QY 181 ATTAAACATGGAATAAAGATTTGTCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240  
Db 181 ATTAAACATGGAATAAAGATTTGTCTTAAATATAATCTACAAGAAGACTTTTGATATTG 240  
QY 241 TTTTTCACAAGTGAAGCATTTCTATAAAGTGTCAATACCTTTTGGGGAAACTATGGGAA 300  
Db 241 TTTTTCACAAGTGAAGCATTTCTATAAAGTGTCAATACCTTTTGGGGAAACTATGGGAA 300  
QY 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGGAACCTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
QY 361 TCTCTTTACAGGAGCTCTCGAGCCCTCACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
Db 361 TCTCTTTACAGGAGCTCTCGAGCCCTCACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
QY 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTGTAGTATCTGTGTATCAAGTATAAA 480  
QY 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526  
Db 481 AGTTCTATAAAGCTGTAGTACTTATTTTAAATCCCAAGCACAGT 526

## RESULT 9

US-10-144-678A-311  
; Sequence 311, Application US/10144678A  
; Publication No. US20030157089A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Deng, Ta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C28  
; CURRENT APPLICATION NUMBER: US/10/144,678A  
; CURRENT FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 1033  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 311  
; LENGTH: 526  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 499  
; OTHER INFORMATION: n = A,T,C or G  
US-10-144-678A-311

Query Match 100.0%; Score 525; DB 7; Length 526;  
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Mismatches 0; Indels 0; Gaps 0;  
Matches 526; Conservative 0;  
Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60  
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60  
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAAGTCCATAAATATATATATCTA 120  
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAAGTCCATAAATATATATATCTA 120  
Qy 121 CATTTCACAGCATTTAAATGTGTTTACAGATGAATATTTAGCTACAGGGAAAGCTAAATAA 180  
Db 121 CATTTCACAGCATTTAAATGTGTTTACAGATGAATATTTAGCTACAGGGAAAGCTAAATAA 180  
Qy 181 ATTAACACATGAATAAAGATTTTGTCTTAAATATAATCTCAAGAAGACTTTTGATATTG 240  
Db 181 ATTAACACATGAATAAAGATTTTGTCTTAAATATAATCTCAAGAAGACTTTTGATATTG 240  
Qy 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTTAAATCTCAAGAAGACTTTTGATATTG 300  
Db 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTTAAATCTCAAGAAGACTTTTGATATTG 300  
Qy 301 AAAATGGGGAAACTCTGGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGGAAACTCTGGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360

Qy 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
Db 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTGTATGATCTGTGTATCAAGATATAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTGTATGATCTGTGTATCAAGATATAA 480  
Qy 481 AGTTCTATAAACTGTAGTACTTATTTTAAATCCCAAGACAGT 526  
Db 481 AGTTCTATAAACTGTAGTACTTATTTTAAATCCCAAGACAGT 526

## RESULT 10

US-10-294-025-311  
; Sequence 311, Application US/10294025  
; Publication No. US20030185830A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolk, John A.  
; APPLICANT: Kalos, Michael D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C29  
; CURRENT APPLICATION NUMBER: US/10/294,025  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 1038  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 311  
; LENGTH: 526  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 499  
; OTHER INFORMATION: n = A,T,C or G  
US-10-294-025-311

Query Match 100.0%; Score 525; DB 7; Length 526;  
Best Local Similarity 100.0%; Pred. No. 6.7e-113; Mismatches 0; Indels 0; Gaps 0;  
Matches 526; Conservative 0;

Qy 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60  
Db 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATTTCTGGGGCCATTTC 60  
Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120  
Db 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATATATATCTA 120  
Qy 121 CATTTCACAGCATTTAAATGTGTTTACAGATGAATATTTAGCTACAGGGAAAGCTAAATAA 180  
Db 121 CATTTCACAGCATTTAAATGTGTTTACAGATGAATATTTAGCTACAGGGAAAGCTAAATAA 180  
Qy 181 ATTAACACATGAATAAAGATTTTGTCTTAAATATAATCTCAAGAAGACTTTTGATATTG 240  
Db 181 ATTAACACATGAATAAAGATTTTGTCTTAAATATAATCTCAAGAAGACTTTTGATATTG 240  
Qy 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTTAAATCTCAAGAAGACTTTTGATATTG 300  
Db 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTTAAATCTCAAGAAGACTTTTGATATTG 300  
Qy 301 AAAATGGGGAAACTCTGGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Db 301 AAAATGGGGAAACTCTGGAAGGGTTTTAGTATCTTACCTGAAGCTACAGACTCCATAACC 360  
Qy 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
Db 361 TCTCTTTACAGGGAGCTCTGCGAGCCCTACAGAAATGAGTGGCTGAGATTTCTTGATTGC 420  
Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTGTATGATCTGTGTATCAAGTATAA 480  
Db 421 ACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTTGTATGATCTGTGTATCAAGTATAA 480



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Query Match          90.9%; Score 477.2; DB 9; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.6e-101;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 CAATTTTCAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 60
Db |||||||
Qy 342 CAATTTTCAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 401
Db |||||||

Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 120
Db |||||||
Qy 402 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 461
Db |||||||

Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAAA 180
Db |||||||
Qy 462 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAAA 521
Db |||||||

Qy 181 ATTAACATGGNAATGAAGATTTGCTTTAAATATATCTACAGAAGACTTTTGATATTG 240
Db |||||||
Qy 522 ATTAACATGGNAATGAAGATTTGCTTTAAATATATCTACAGAAGACTTTTGATATTG 581
Db |||||||

Qy 241 TTTTTCACAAAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
Db |||||||
Qy 582 TTTTTCACAAAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 641
Db |||||||

Qy 301 AAAATGGGAAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db |||||||
Qy 642 AAAATGGGAAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 701
Db |||||||

Qy 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
Db |||||||
Qy 702 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 761
Db |||||||

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTATCAAGTATAAA 480
Db |||||||
Qy 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTATCAAGTATAAA 819
Db |||||||

Qy 481 AGTTCTATAAACTGTAGTACTTATTTAATCCCAA 518
Db |||||||
Qy 820 AGTTCTATAAACTGTAGT-TACTTATTTAATCCCAA 856
Db |||||||
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```
RESULT 13
US-10-357-930-22535
; Sequence 22535, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22535
```

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LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-22535

Query Match          90.9%; Score 477.2; DB 9; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.6e-101;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 CAATTTTCAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 60
Db |||||||
Qy 342 CAATTTTCAGGCAATGACATAGATTTTACAAATCAAGAAGCTTATTCGGGGCCATTTC 401
Db |||||||

Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 120
Db |||||||
Qy 402 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAATTAATTAATCTA 461
Db |||||||

Qy 121 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAAA 180
Db |||||||
Qy 462 CATTTACAGCATTTAAATGTGTTTCAGCATGAATATTTAGCTACAGGGGAAGCTAAATAAA 521
Db |||||||

Qy 181 ATTAACATGGNAATGAAGATTTGCTTTAAATATATCTACAGAAGACTTTTGATATTG 240
Db |||||||
Qy 522 ATTAACATGGNAATGAAGATTTGCTTTAAATATATCTACAGAAGACTTTTGATATTG 581
Db |||||||

Qy 241 TTTTTCACAAAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 300
Db |||||||
Qy 582 TTTTTCACAAAGTGAAGCAATCTTTATAAAGTGTCTATAACCTTTTGGGGAAACTATGGGAA 641
Db |||||||

Qy 301 AAAATGGGAAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360
Db |||||||
Qy 642 AAAATGGGAAACTCTGAAGGGTTTTAAAGTATCTTACCTGAAGCTACAGACTCCATAACC 701
Db |||||||

Qy 361 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 420
Db |||||||
Qy 702 TCTCTTTACAGGAGCTCTCGAGCCCTACAGAAATGAGTGGCTGAGATCTTGATTGC 761
Db |||||||

Qy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTATCAAGTATAAA 480
Db |||||||
Qy 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTAAAGTATCTGTATCAAGTATAAA 819
Db |||||||

Qy 481 AGTTCTATAAACTGTAGTACTTATTTAATCCCAA 518
Db |||||||
Qy 820 AGTTCTATAAACTGTAGT-TACTTATTTAATCCCAA 856
Db |||||||
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```
RESULT 14
US-10-357-930-27610
; Sequence 27610, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
```

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; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62332
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27610
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-27610

Query Match          90.9%; Score 477.2; DB 9; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.6e-101;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATCTCTGGGCCCATTTTC 60
DB 342 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATCTCTGGGCCCATTTTC 401

QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 120
DB 402 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 461

QY 121 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
DB 462 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 521

QY 181 ATTAACATGGAATTAAGATTTGTCCTTAAATATAATCTACAAGAGACTTTTGATATTG 240
DB 522 ATTAACATGGAATTAAGATTTGTCCTTAAATATAATCTACAAGAGACTTTTGATATTG 581

QY 241 TTTTTCACAGGAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 300
DB 582 TTTTTCACAGGAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 641

QY 301 AAAATGGGAAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 360
DB 642 AAAATGGGAAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 701

QY 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
DB 702 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 761

QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGATCAAGTATAA 480
DB 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGATCAAGTATAA 819

QY 481 AGTCTATAAAGCTAGTNTACTTATTTTAAATCCCCAA 518
DB 820 AGTCTATAAAGCTAGT-TACTTATTTTAAATCCCCAA 856

RESULT 15
US-10-357-930-28370
; Sequence 28370, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
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; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62332
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28370
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28370

Query Match          90.9%; Score 477.2; DB 9; Length 1203;
Best Local Similarity 98.8%; Pred. No. 1.6e-101;
Matches 512; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATCTCTGGGCCCATTTTC 60
DB 342 CAAATTTGAGCCCAATGACATAGAAATTTTACAAATCAAGAGCTTATCTCTGGGCCCATTTTC 401

QY 61 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 120
DB 402 TTTTGACGTTTCTCTAAACTACTAAAGAGGCAATTAATGATCCATAAAATTTATATTATCTA 461

QY 121 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
DB 462 CATTTACAGCAATTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 521

QY 181 ATTAACATGGAATTAAGATTTGTCCTTAAATATAATCTACAAGAGACTTTTGATATTG 240
DB 522 ATTAACATGGAATTAAGATTTGTCCTTAAATATAATCTACAAGAGACTTTTGATATTG 581

QY 241 TTTTTCACAGGAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 300
DB 582 TTTTTCACAGGAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 641

QY 301 AAAATGGGAAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 360
DB 642 AAAATGGGAAACTCTGAAGGGTTTTAAGTATCTTAACTGAAGCTACAGACTCCATAAC 701

QY 361 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420
DB 702 TCTCTTTACAGGAGCTCTGAGCCCTTACAGAAATGAGTGGCTGAGATTCTTGATTGC 761

QY 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGATCAAGTATAA 480
DB 762 ATAGC-AGAGCTTCTCATCTAAACCTTTCCCTTTTATAGTATCTGATCAAGTATAA 819

QY 481 AGTCTATAAAGCTAGTNTACTTATTTTAAATCCCCAA 518
DB 820 AGTCTATAAAGCTAGT-TACTTATTTTAAATCCCCAA 856

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Job time : 839.563 secs
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GenCore version 5.1.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2006, 12:14:13 ; Search time 4216.27 Seconds  
(without alignments)  
6976.201 Million cell updates/sec

Title: US-09-232-880-311

Perfect score: 525

Sequence: 1 caaatgagccaatgacat.....tttaatcccaagcacagt 526

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_ges1:\*  
12: gb\_ges2:\*  
13: gb\_ges3:\*  
14: gb\_ges4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	361.4	68.8	684	14 AG130449	AG130449 Pan trogl
C 2	335	63.8	678	14 AG093969	AG093969 Pan trogl
C 3	289	55.0	478	11 AQ015128	AQ015128 CIT-HSP-2
C 4	224.2	42.7	597	4 BX098119	BX098119 EX098119
C 5	216.2	41.2	524	1 AA843706	AA843706 aj42f05.s
C 6	178.2	33.9	360	10 R82378	R82378 Yj18b01.r1
C 7	166.8	31.8	301	7 BE694624	BE694624 PMO-BT075
C 8	145.2	27.7	462	1 AA528286	AA528286 nh26d07.s
C 9	144.2	27.5	288	7 BE827798	BE827798 RC2-ET002
C 10	144.2	27.5	554	7 BF001177	BF001177 tg59c10.x
C 11	126.8	24.2	265	1 AA525072	AA525072 nh32h04.s
C 12	124	23.6	559	11 AQ802217	AQ802217 HS 3167 B
C 13	122.4	23.3	577	4 CB049577	CB049577 NISC gj11
C 14	110.6	21.1	434	12 CE393091	CE393091 tigr-g88-
C 15	87	16.6	709	14 AG056821	AG056821 Pan trogl
C 16	60	11.4	298	14 AG201193	AG201193 Pan trogl
C 17	58.2	11.1	432	7 AW971282	AW971282 EST38371
C 18	56.8	10.8	808	11 B2499226	B2499226 BONIL22TF
C 19	56.8	10.8	866	7 BF678216	BF678216 602086120

20 56.8 10.8 997 11 BZ433986  
21 55.2 10.5 391 1 AA969621  
22 53.4 10.2 1092 14 CNS020K7  
23 52 9.9 1101 14 CNS00PMC  
24 51 9.7 118 14 AG201107  
25 50.8 9.7 710 14 AG368405  
26 50.8 9.6 1101 14 CNS016LI  
27 50.4 9.6 1043 14 CNS0145P  
28 50.2 9.6 971 13 DU092632  
29 50.2 9.6 1406 11 BZ563321  
30 50 9.5 1101 14 CNS00EVL  
31 50 9.5 1272 12 CC264939  
32 49.8 9.5 987 14 CNS014PQ  
33 49.8 9.5 1101 14 CNS00EVL  
34 49.6 9.4 811 11 BH689045  
35 49.6 9.4 1101 14 CNS003BD  
36 49 9.3 450 9 DN469325  
37 48.6 9.3 910 14 AG526131  
38 48.4 9.2 1101 14 CNS0039G  
39 48 9.1 1101 14 CNS00FVE  
40 47.6 9.1 696 13 DU002903  
41 47.6 9.1 826 14 DX023921  
42 47.4 9.0 501 11 AZ606637  
43 47.4 9.0 1165 1 AJ928354  
44 47.2 9.0 642 11 AZ606553  
45 47.2 9.0 849 14 CR163197

#### ALIGNMENTS

RESULT 1  
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LOCUS AG130449 684 bp DNA linear GSS 04-NOV-2001  
DEFINITION Pan troglodytes DNA, clone: PTB-142D13.F, genomic survey sequence.  
ACCESSION AG130449  
VERSION AG130449.1 GI:16659614  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE 1  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE BAC end sequences of Library PTB  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 684)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimo-Ogino, Tsukuba, Ibaraki, Japan, 305-8565, Japan

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Best Local Similarity 97.1%; Pred. No. 6.4e-74;
Matches 368; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
Db 456 CAAATTTGATCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCAGTTC 397
Qy 61 TTTTGACGTTTTCTCTAACTACTAAAGAGCAATTAATGATCCATAAATATATATCTA 120
Db 396 TTGTGACGTGTTCTCTAACTACTAAAGAGCAATTAATGATCCATAAATATATATCTA 337
Qy 121 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 336 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAAATATTAGCTACAGTGGAGCTAAATAA 277
Qy 181 ATTTAAACATGGAATAAAGATTGTCTCTTAAATATATCTACAAAGAAGCTTTGATATTG 240
Db 276 ATTTAAACATGGAATAAAGATTGTCTCTTAAATATATCTACAAAGAAGCTTTGATATTG 217
Qy 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCAATGCTTTTGGGGAAGCTATGGAA 300
Db 216 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCAATGCTTTTGGGGAAGCTATGGAA 157
Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGATCCATAACC 360
Db 156 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGATCCATAACC 97
Qy 361 TCTCTTTACAGGAGCTCC 379
Db 96 TCTCTTTACAGGAGCTCC 78

RESULT 2
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LOCUS      AG093969      678 bp      DNA      linear      GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-094J13.F, genomic survey sequence.
ACCESSION  AG093969
VERSION     AG093969.1 GI:16645771
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Pan.
REFERENCE  1
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library PTB
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 678)
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimbasesgc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT    Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector      : pKSI45
R.Site 1    : SacI
R.Site 2    : SacI
            Location/Qualifiers

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Matches 358; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

Qy 1 CAAATTTGAGCCAATGACATAGAAATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
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Qy 61 TTTTGACGTTTTCTCTAACTACTAAAGAGCAATTAATGATCCATAAATATATATCTA 120
Db 400 TTTTGATGTTTTCTCTAACTACTAAAGAGCAATTAATGATCAATGAATATATATCTA 341
Qy 121 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 340 CATTTTACAGCATTTTAAATGTGTTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 281
Qy 181 ATTTAAACATGGAATAAAGATTGTCTCTTAAATATATCTACAAAGAAGCTTTGATATTG 240
Db 280 ATTTAAATATGGAATAAAGATTGTCTCTTAAATATATCTACAAAGAAGCTTTGATATTG 221
Qy 241 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGAA 300
Db 220 TTTTTCACAGTGAAGCATTTCTTATAAGTGTCTATAACCTTTTGGGGAAGCTATGGG-G 162
Qy 301 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGATCCATAACC 360
Db 161 AAAATGGGGAACCTCTGAAGGGTTTTTAAGTATCTTACCTGAAGCTACAGATCCATAACC 102
Qy 361 TCTCTTTACAGGAGCTCC 379
Db 101 TCTCTTTACAGGAGCTCC 83

RESULT 3
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LOCUS      AQ015128      478 bp      DNA      linear      GSS 09-JUN-1998
DEFINITION CIT-HSP-2301D2.TF CIT-HSP Homo sapiens genomic clone 2301D2,
            genomic survey sequence.
ACCESSION  AQ015128
VERSION     AQ015128.1 GI:3193864
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 478)
AUTHORS    Adams,M.D., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
            Golden,K., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
            Simon,M. and Venter,J.C.
TITLE      Use of a random BAC End Sequence Database for Sequence-Ready Map
            Building (1998)
JOURNAL    Unpublished (1998)
COMMENT    Other GSSs: CIT-HSP-2301D2.TR
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:

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Figure 1. The effect of the number of trials on the number of correct responses.

Email: [cgapps-remail.n](mailto:cgapps-remail.n)  
cDNA Library Preparation

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image.html](http://www-bio.llnl.gov/bbrp/image.html)  
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 Location/Qualifiers  
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## FEATURES

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/clone_lib="Soares testis NHT"
/note="Vector: pT73D-PacI; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was prepared from mRNA obtained from
Clontech Laboratories, Inc., and primed with a Not I -
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TGTTACCAATCTGAAGTCGAGCGGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

## ORIGIN

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Query Match      41.2%; Score 216.2; DB 1; Length 524;
Best Local Similarity 98.6%; Pred. No. 6.3e-40;
Matches 218; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAATTTGAGCCCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 60
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QY 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATTTATATCTA 120
Db 364 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATTTATCTA 423

QY 121 CATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
Db 424 CATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 483

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RESULT 6
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IMAGE:149065 5', mRNA sequence.
ACCESSION R82378
VERSION   R82378.1 GI:861769
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 360)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marr,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
```

Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 694  
 High quality sequence stops: 238  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
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## FEATURES

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strand cDNA was primed with a Not I - oligo(dT) primer [5',
AATCGAAGAAATTCGGCGCGCAGGAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "
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## ORIGIN

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Query Match      33.9%; Score 178.2; DB 10; Length 360;
Best Local Similarity 95.1%; Pred. No. 4.8e-31;
Matches 195; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 2 AAAATTTGAGCCCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGCCATTTC 61
Db 203 AATTTGAGCCCAATGACATAGATTTTACAAATCAAGAAGCTTATCTGGGGC--ATTTC 146

QY 62 TTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATTTATATCTAC 121
Db 145 TTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAAATGATCCATAAATTTATATCTAC 86

QY 122 ATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 181
Db 85 ATTTACAGCATTTAAATGTGTTCCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 26

QY 182 TTAACATGGAATAAAGATTGTGCC 206
Db 25 TTAACATGGAATAAAGATTGTGCC 1
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RESULT 7
BE694624
LOCUS      PMO-BT0757-240500-003-D01 BT0757 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE694624
ACCESSION  BE694624
VERSION    BE694624.1 GI:10081784
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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```

REFERENCE
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 301)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
```

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=PMO-BT0757-240  
500-003-D01&t3=2000-05-24&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 301.

#### FEATURES

Location/Qualifiers  
1..301  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="BT0757"  
/notes="Organ: breast; Vector: puc18; Site\_1: Smal; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

#### ORIGIN

Query Match 31.8%; Score 166.8; DB 7; Length 301;  
Best Local Similarity 93.2%; Pred. No. 2.2e-28;  
Matches 207; Conservative 0; Mismatches 12; Indels 3; Gaps 3;  
QY 297 GGAAAAAATGGGAACTCTGAAGGTTTTTAAGTATCTTACCTGAAGCTACAGACTCCAT 356  
|||||  
Db 5 GGAGAAATGGGAAACTCTGAAGGTTTTTAAGTACCTTTCTGGAAGCTCGAGACTCCAT 64  
QY 357 AACCTCTTTACAGGAGCTCTCGAGCCCTTACAGAAATGAGTGGCTGAGATTTCTGA 416  
|||||  
Db 65 AACCTCTTTACAAAGAGCTCTCGAGCTCTTACAGAAATGAGTGGCTGAGATTTCTGA 124  
QY 417 TTGCACAGCAAGAGCTTCTCATCTAAACCTTTTCCCTTTTCTAGTATCTGTATCAAGTA 476  
|||||  
Db 125 TTGCATAGC-AGAGCTTCTCATCTAAACCTTTTCCCTTTTCTAGTATCTGTATC-AGTA 182  
QY 477 TAAAGTTCTATAAAGCTAGTACTTATTTTAAATCCCAAA 518  
|||||  
Db 183 TAAAGTTCTATAAAGCTAGT-TACTTATTTTAAATCCCAAA 223

RESULT 8  
AA528286/c  
LOCUS  
DEFINITION  
AA528286 462 bp mRNA linear EST 05-AUG-1997  
nh26d07.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:953485, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 462)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

#### JOURNAL COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 890 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 325.

#### FEATURES

Location/Qualifiers  
1..462  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:953485"  
/sex="Male"  
/dev\_stage="45 years old"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP\_Pr3"  
/note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

#### ORIGIN

Query Match 27.7%; Score 145.2; DB 1; Length 462;  
Best Local Similarity 91.6%; Pred. No. 2.6e-23;  
Matches 175; Conservative 0; Mismatches 14; Indels 2; Gaps 2;  
QY 328 AGTATCTTACCTGAAGCTACAGACTCCATAACCTCTTTTACAGGAGCTCTCGAGCCC 387  
|||||  
Db 434 AGTGGTTCCCTGAAGCTACAGACTCCATAACCTCTTTAGAGGAGCTCTCGAGCCC 375  
QY 388 CTACAGAAATGAGTGGCTGAGATTCTTGATTGCACAGCAAGAGCTTCTCATCTAAACCT 447  
|||||  
Db 374 ATACAGAAATGAGTGGCTGAGATTCTTGATTGCATAGC-AGAGCTTCTCATCTAAACCT 316  
QY 448 TTCCCTTTTCTAGTATCTGTGTATCAAGTATAAAGTTCTATAAAGTGTAGTACTATT 507  
|||||  
Db 315 TTCCCTTTTCTAGTGTCTGTATC-AGTATAAAGTTCTATAAAGTGTAGTACTATT 257  
QY 508 TTAATCCCAAA 518  
|||||  
Db 256 TTAATCCCAAA 246

#### RESULT 9

BE827798  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 288)  
BE827798 288 bp mRNA linear EST 22-SEP-2000  
RC2-ET0022-170500-015-all ET0022 Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 288)

**AUTHORS** Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

**PUBMED** 10737800

**COMMENT** Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel.: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC2-ET0022-170500-015-all&t3=2000-05-17&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 17  
High quality sequence stop: 288.

**FEATURES** source  
Location/Qualifiers

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ET0022"  
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 27.5%; Score 144.2; DB 7; Length 288;  
Best Local Similarity 96.8%; Pred. No. 4.3e-23;  
Matches 179; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 334 TTACTCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGGAGCTCCTGCAGGCCCTACAG 393  
|||||  
Db 88 TTACTCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGAGCTCTCGAGGCCCTACAG 147  
|||||

Qy 394 AAATGAGTGGCTGAGATCTTGATTGCACAGCAGAGCTTCTCATCTAAACCCCTTCCCT 453  
|||||

Db 148 AAATGAGTGGCTGAGATCTTGATTGCACAGC-AGAGCTTCTCATCTAAACCCCTTCCCT 206  
|||||

Qy 454 TTTTAGTATCTGTGTATCAAGTATATAAAGTCTATATAAGTCTAGTNTACTTTTAAATC 513  
|||||

Db 207 TTTTAGTCTGTGTATC-AGTATAAAGTCTATAAAGTCTATAAAGTCTAGT-TACTTATTTTAAATC 264  
|||||

Qy 514 CCCAA 518  
|||

Db 265 CCAAA 269  
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**RESULT 10**  
BF001177  
**LOCUS** BF001177  
**DEFINITION** 7959c10.x1 NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:3110770 3', mRNA sequence.  
BF001177  
**ACCESSION** BF001177  
**VERSION** BF001177.1 GI:10701452  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 554)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
**AUTHORS** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**TITLE** Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-f@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 432.

**FEATURES** source  
Location/Qualifiers

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:3110770"  
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/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Pr28"  
/note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA  
from the normalized library NCI CGAP Pr22 was prepared,  
and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneIDs 985608-986759, 1101192-1101959, and  
1217928-1220615). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

## ORIGIN

Query Match 27.5%; Score 144.2; DB 7; Length 554;  
Best Local Similarity 96.8%; Pred. No. 4.6e-23;  
Matches 179; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 334 TTACTCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGGAGCTCCTGCAGGCCCTACAG 393  
|||||

Db 325 TTACTCTGAAGCTACAGACTCCATAACCTCTCTTTACAGGAGCTCCTGCAGGCCCTACAG 384  
|||||

Qy 394 AAATGAGTGGCTGAGATCTTGATTGCACAGCAGAGCTTCTCATCTAAACCCCTTCCCT 453  
|||||

Db 385 AAATGAGTGGCTGAGATCTTGATTGCATAGC-AGAGCTTCTCATCTAAACCCCTTCCCT 443  
|||||

Qy 454 TTTTAGTATCTGTGTATCAAGTATATAAAGTCTATAAAGTCTAGTNTACTTTTAAATC 513  
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Db 444 TTTTAGTCTGTGTATC-AGTATAAAGTCTATAAAGTCTAGT-TACTTATTTTAAATC 501  
|||||

Qy 514 CCCAA 518  
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Db 502 CCAAA 506  
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**RESULT 11**  
AA525072/c  
**LOCUS** AA525072  
**DEFINITION** nh32h04.b1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:954103, mRNA  
sequence.  
AA525072  
**ACCESSION** AA525072  
**VERSION** AA525072.1 GI:2266000  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

REFERENCE  
 1 (bases 1 to 265)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,  
 M.D., Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Seq primer: -40m13 fwd. RT from Amersham.

#### FEATURES

Location/Qualifiers  
 1..265  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:954103"  
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 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr3"  
 /note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (life technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

#### ORIGIN

Query Match 24.2%; Score 126.8; DB 1; Length 265;  
 Best Local Similarity 97.9%; Pred. No. 5e-19;  
 Matches 139; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 QY 334 TTACCTGAGCTACAGACTCCATAACCTCTTTACAGGAGCTCTCGAGCCCTACAG 393  
 DB 146 TTACCTGAGCTACAGACTCCATAACCTCTTTACAGGAGCTCTCGAGCCCTACAG 87  
 QY 394 AATAGTGGCTGAGATTCTTGATTCACAGCAAGAGCTTCTCATCTAAACCCCTTCCCT 453  
 DB 86 AATAGTGGCTGAGATTCTTGATTCACAGC-AGAGCTTCTCATCTAAACCCCTTCCCT 28  
 QY 454 TTTTAGTATCTGTGTATCAAGT 475  
 DB 27 TTTTAGTGTGTGTATCAGGT 6

#### RESULT 12

AQ802217/c  
 LOCUS  
 DEFINITION  
 HS\_3167\_B2\_D11\_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3167 Col=22 Row=H, genomic survey sequence.  
 ACCESSION  
 AQ802217  
 VERSION  
 AQ802217.1 GI:5719549  
 KEYWORDS  
 GSS.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 559)

#### AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kellier,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

#### TITLE

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

#### JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

#### COMMENT

10449764  
 Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: [jwallace@u.washington.edu](mailto:jwallace@u.washington.edu)  
 Clones may be purchased from Research Genetics ([info@resgen.com](mailto:info@resgen.com)).  
 BAC end Web Server: <http://www.htsc.washington.edu>  
 Plate: 3167 row: H Column: 22  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 559.

#### FEATURES

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=3167 Col=22 Row=H"  
 /sex="male"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

#### ORIGIN

Query Match 23.6%; Score 124; DB 11; Length 559;  
 Best Local Similarity 91.1%; Pred. No. 2.5e-18;  
 Matches 163; Conservative 0; Mismatches 13; Indels 3; Gaps 3;  
 QY 337 CCTGAAGCTACAGACTCCATAACCTCTTTACAGGAGCTCTCGAGCCCTACAGAAA 396  
 DB 553 CCTGAAGATGCAGACTCCATAACCTCTTTACANAGAGCTCTGAGCTCATACAGAGA 494  
 QY 397 TGAGTGGCTGAGATTCTTGATTCACAGCAAGAGCTTCTCATCTAAACCCCTTCCCTTTT 456  
 DB 493 TGAGTGGCTGAGATTCTTGATGACATAGC-AGAGCTTCTCATCTAAACCCCTTCCCTTTT 435  
 QY 457 TAGTATCTGTGTATCAAGTATATAAGTCTCTATAAACTAGTNTACTTATTTTAAATCCC 515  
 DB 434 TAGTGTGTGTATC-AGTATAAAAGTCTCTATAAACTGTAGT-TACTTATTTTAAATCCC 378

#### RESULT 13

CB049577  
 LOCUS  
 DEFINITION  
 NISC G111g01.x1 NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:3271488 3', mRNA sequence.  
 ACCESSION  
 CB049577  
 VERSION  
 CB049577.1 GI:27787864  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 577)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 cDNA Library Preparation:  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
 Plate: L1AM8008 row: N column: 1  
 Seq primer: -21M13 forward primer (ABI).  
 Location/Qualifiers

## FEATURES

1..577  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3271488"  
 /sex="male"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr28"  
 /notes="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 23.3%; Score 122.4; DB 4; Length 577;  
 Best Local Similarity 89.7%; Pred. No. 5.9e-18;  
 Matches 165; Conservative 0; Mismatches 16; Indels 3; Gaps 3;  
 Qy 334 TTACTGAGCTACAGATCCATACCTCTCTTTACAGGGAGCTCTCGACGCCCTACAG 393  
 Db 397 TTACTGAACTACAACTCCATACCTTTTTTTACAGGGAGCTCTCGACGCCCTACAA 456  
 Qy 394 AAATGAGTGGCTGAGATCTTGATTGCACAGCAGAGCTTCTCATCTAAACCTTTCCCT 453  
 Db 457 AAATGAGTGGCTGAAATTTTGAATGCAACAA- AACTTTTCATCTAAACCTTTCCCT 515  
 Qy 454 TTTTAGTATCTGTGTATCAAGTATATAAAGTTCTATATAAAGTGTAGTNTACTTTTAAATC 513  
 Db 516 TTTTAGGGCTGGGTATCAAA-AATAAAGTTCTATAAACTGTAGT-TACTATTTTAATC 573  
 Qy 514 CCCA 517  
 Db 574 CCAA 577

## RESULT 14

CE393091/c  
 LOCUS  
 DEFINITION  
 tigr-gss-dog-17000334478329 Dog library Canis familiaris genomic,  
 genomic survey sequence.

CE393091  
 ACCESSION  
 CE393091.1 GI:36634243

VERSION  
 GSS.

KEYWORDS  
 SOURCE

ORGANISM  
 Canis familiaris (dog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

## REFERENCE

1 (bases 1 to 434)  
 Kirckness, E.F., Baina, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.

The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)

14512627

## COMMENT

Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1..434  
 /organism="Canis familiaris"  
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 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
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## ORIGIN

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 Qy 1 CAAATTTGAGCAATGATAGATAATTTTACAA-ATCAAGAAGCTTTATTTCTGGGCCCATTT 59  
 Db 253 CAACTTGTAGTTAATGCGACAGAAATTTTACAAGATCAAAAAGCTTTCATCTAGAGCCATTT 194  
 Qy 60 CTTTGTGACGTTTCTCTAAACTACTAAAGAGGC-ATTAAATGATCCATAAATATATATATC 118  
 Db 193 CTTTTTAAGTTCTTCTTAAGCTACTCAAGAGGCAACTGTTTCTCCATAAATATATATCATC 134  
 Qy 119 TACATTTACAGCATT-----TAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAA 171  
 Db 133 TACCTTTTACAGGATTAATAAAAAAATGTTGGGCATGCAACATTAGCCTCAGTGTTA 74  
 Qy 172 GCTAAATAAATTAACATCGAATAAGATTGTCTCTTAAATATAATCTTACAAGAAGACTT 231  
 Db 73 GCTAAGTAAATTAACAGGGAATAAGCTTTGATCTTAAATAATCATTACCAGAAAGATCT 14  
 Qy 232 TGATATTTGTTTT 244  
 Db 13 TAATATTTGTTTT 1

## RESULT 15

AG056621  
 LOCUS  
 DEFINITION  
 Pan troglodytes DNA, clone: PTB-042P10.F, genomic survey sequence.

AG056621  
 ACCESSION  
 AG056621.1 GI:16594080

VERSION  
 GSS.

KEYWORDS  
 SOURCE

ORGANISM  
 Pan troglodytes (chimpanzee)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Pan.

## REFERENCE

1  
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library PTB

Unpublished

2 (bases 1 to 709)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/;

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the R&D process and may have higher chance of  
 clone tracking errors.

## PRIMERS

Sequencing: -21M13

## LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI.



FEATURES

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Location/Qualifiers  
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/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

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Db 64 GATCATACGCGTTTCGAAAGCTTCGCGACGTCCGCGAGCTCTGCAGAAATGA 123  
QY 400 GTGGCTGAGATTCTTGATTGCACAGCAAGAGCTTCTCATCTAAACCCCTTTCCCTTTTAG 459  
|||  
Db 124 GTGGCTGAGATTCTGTGTCATAGC-AGAGCTTCTCATCCAAACCCCTTTCCCTTTTAG 182  
QY 460 TATCTGTGTATCAAGTATAAAAGTTCTATAAACTGTAGTNTACTTATTTTAATCCCAA 518  
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Db 183 TGTCTGTGTATC-AGTATAAAGTTCTATAAACAGTAGT-TACTTATTTTAATCCCAA 239

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